



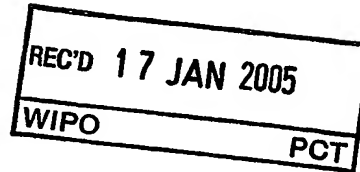
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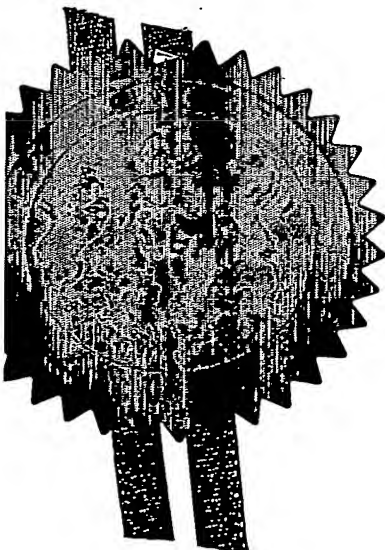
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**22 DEC 2003**

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Glaxo Group Limited  
Glaxo Wellcome House, Berkeley Avenue,  
Greenford, Middlesex UB6 0NN, Great Britain

**473587003**  
United Kingdom

4. Title of the invention

Method

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### Priority Documents

Translations of priority documents

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Request for preliminary examination and search (*Patents Form 9/77*)

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We request the grant of a patent on the basis of this application

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## Method

### Field of the Invention

This invention relates to methods of modulating the proteolytic processing  
5 of amyloid precursor protein (APP) and methods of treatment of conditions in  
which abnormal processing of amyloid precursor protein (APP) is implicated such  
as Alzheimer's disease.

### Background to the Invention

10 Alzheimer's disease (AD) is characterised by the presence of two  
diagnostic features of pathology. These are amyloid plaques and neurofibrillary  
tangles composed of aggregated beta-amyloid peptide (A $\beta$ 40 and A $\beta$ 42) and  
hyperphosphorylated tau respectively (Dawbarn & Allen 2001 Neurobiology of  
Alzheimer's Disease OUP).

15 A comprehensive study has shown a strong link in patients between beta-  
amyloid accumulation and cognitive decline (Naslund et al 2000). This is  
consistent with genetic and epidemiological studies that suggest that some  
mutations in APP and presenilin genes can predispose to early onset AD, which  
mutations also enhance the levels of A $\beta$ 40 and A $\beta$ 42 peptide, including the ratio  
20 thereof.

Cleavage of the type I transmembrane amyloid precursor protein (APP)  
by two distinct proteases designated beta- and gamma-secretase is necessary  
for the formation of beta-amyloid peptide. The molecular identity of beta-  
secretase as the aspartyl-protease Asp2/BACE1 has been confirmed (Hussain et  
25 al 1999; Vassar et al 1999). The nature of gamma-secretase remains the source  
of some debate and is likely to consist of a high molecular weight complex  
consisting of at least the following proteins: presenilins, Aph1, Pen2 and nicastrin  
(reviewed in Medina & Dotti Cell Signalling 2003 15(9):829-41).

The processing of APP within the CNS is likely to occur within a number  
30 of cell-types including neurons, oligodendrocytes, astrocytes and microglia. While  
the overall rate of APP processing in these cells will be influenced by the relative  
level of expression of APP, BACE1/Asp2, presenilin-1 and -2, Aph1, Pen2 and  
nicastrin.

Furthermore, additional factors regulating the subcellular location of APP can also influence its processing as shown by the finding that mutation of the YENP motif in the APP cytoplasmic domain which blocks its endocytosis reduces beta-amyloid production (Perez et al 1999 J Biol Chem 274 (27) 18851-6).

5 Retention of the APP-beta-CTF in the ER by the addition of the KKQN retention motif is sufficient to reduce amyloid production in transfected cells (Maltese et al 2001 J Biol Chem 276 (23) 20267-20279). Conversely, elevation of endocytosis, by overexpression of Rab5 is sufficient to elevate amyloid secretion from transfected cells (Grbovic et al 2003 J Biol Chem 278 (33) 31261-31268).

10 Consistent with these findings further studies have shown that reduction of cellular cholesterol levels (a well known risk factor for AD) reduced beta-amyloid formation. This change was dependent on altered endocytosis as demonstrated by the use of the dominant negative dynamin mutants (K44A) and overexpression of the Rab5 GTPase activating protein RN-Tre (Ehehalt et al  
15 2003 J Cell Biol 160 (1) 113-123).

Cholesterol rich microdomains or rafts are also an important cellular site of beta-amyloid production and APP, BACE1 and components of the gamma-secretase complex have all been shown to transiently reside within rafts. Antibody cross-linking of APP and BACE1 towards cholesterol rich rafts was able  
20 to elevate beta-amyloid production (Ehehalt et al 2003 J Cell Biol 160 (1) 113-123). Expression of GPI-anchored BACE1, which is exclusively targeted to lipid rafts, is similarly able to elevate APP cleavage and beta-amyloid production (Cordy et al 2003 PNAS 100(20) 11735-11740).

Neuronal growth is finely balanced by the activities of positive factors  
25 such as neurotrophins like NGF and matrix proteins like laminin and the opposing activities of inhibitory factors such as ephrins, MAG, semaphorin-3A and Nogo-A (reviewed in Tessier-Lavigne & Goodman 2000 Science 287(5454):813-4). The antagonistic nature of the signalling from these factors is illustrated by the finding that enhanced neuronal growth correlates with a reduction in RhoA activation  
30 (Nusser et al 2002 J Biol Chem 277 (39) 35840) and the inhibition of neuronal growth results in increased RhoA activation (Niederost et al 2002 J Neuroscience 22(23) 10368-10376).

NOGO is a protein found in the myelin sheath that has inhibitory action on axonal growth (Prinjha, R et al (2000) Nature 403, 383-384; GrandPre, T et al (2000) Nature 403, 439-444 and Chen, MS et al (2000) Nature 403, 434-439).

At least three Nogo isoforms are generated by alternative splicing of transcripts derived from the NogoA gene. The C-terminal third of all three isoforms shares high homology (approximately 70% at the amino acid level) with the reticulon protein family. NogoA, the largest isoform, has been shown to inhibit axon regeneration in culture. It is thought that the normal role of Nogo proteins is to prevent axon sprouting in the uninjured central nervous system. NogoA is localised to central nervous system myelin and is highly expressed in oligodendrocytes; NogoB and NogoC are expressed in some neurons and several non-neural tissues. All Nogo isoforms surprisingly have a C-terminal ER-retention motif but at least some of NogoA protein is thought to reach the cell surface. All 3 Nogo isoforms have 2 potential trans-membrane domains. Both the C and N termini may be cytoplasmically exposed and a 66 amino acid loop separated by the TM domains may be located extracellularly.

It has been reported that BACE and NOGO may interact in a physical sense, but such reports are based solely on immunoprecipitation experiments (for example WO02/058323 and WO03/088926). There has been no further confirmation of this proposed physical interaction and no experimental evidence of any functional interaction between BACE and NOGO.

The process of neurodegeneration underlies many neurological diseases/disorders including, but not limited to, acute diseases such as stroke, traumatic brain injury and spinal cord injury as well as chronic diseases including Alzheimer's disease, fronto-temporal dementias (tauopathies), peripheral neuropathy, Parkinson's disease, Huntington's disease, Creutzfeldt-Jakob Disease (CJD), multiple sclerosis and inclusion body myositis.

The identification of therapeutic and prophylactic treatments for neurodegenerative diseases, in particular Alzheimer's disease, remains a highly desirable goal for the pharmaceutical industry and for healthcare providers.

### Summary of the Invention

The present invention is based on the finding that antagonists of NOGO influence the production of the amyloidogenic A $\beta$  peptide. This novel finding provides an unexpected route for therapeutic intervention in disorders resulting from abnormal production of A $\beta$  peptide in particular Alzheimer's disease.

5       Accordingly the invention provides a method of modulating A $\beta$  peptide production using an antagonist of NOGO. Further the invention provides methods of modulating BACE activity, methods of modulating amyloid deposition, pharmaceutical compositions and methods for the treatment of neurodegenerative diseases such as Alzheimer's disease.

10

#### **Detailed description of the invention**

In a preferred aspect the invention provides a method of modulating production of an amyloidogenic peptide comprising contacting a cell which is expressing:

- 15       a) the precursor from which the amyloidogenic peptide is derived; and  
      b) a NOGO polypeptide  
      with a NOGO antagonist.

      In a preferred embodiment the precursor is APP. Preferably the amyloidogenic peptide is A $\beta$ , most preferably A $\beta$ 40, A $\beta$ 42 or a combination of  
20       both.

      In a further preferred embodiment the NOGO polypeptide is NOGO-A.

      The NOGO antagonist may be a small organic molecule, peptide, polypeptide or antibody that binds to NOGO and thereby inhibits or extinguishes NOGO activity. Other possible NOGO antagonists include peptides,  
25       polypeptides, oligonucleotides or polynucleotides (for example aptamers) that binds to the same site on the NOGO receptor molecule as the NOGO polypeptide, but without inducing NOGO receptor-induced activities, thereby preventing the action of the NOGO receptor by excluding NOGO from binding.

      Further potential antagonists include small molecules which bind to and  
30       occupy a binding site on the NOGO polypeptide thereby preventing binding to cellular binding molecules, such as receptor molecules, such that normal NOGO biological activity is prevented or reduced. Examples of such small molecules include, but are not limited to small organic molecules, peptides or peptide-like

molecules, polypeptides, oligonucleotides or polynucleotides (for example aptamers).

In still another approach, expression of the gene encoding endogenous NOGO polypeptide can be inhibited using expression blocking techniques.

5 Known such techniques involve the use of antisense sequences, either internally generated or separately administered (see, for example, O'Connor, J Neurochem (1991) 56:560 in Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Alternatively, oligonucleotides which form triple helices ("triplexes") with the gene can be supplied (see, for  
10 example, Lee *et al.*, Nucleic Acids Res (1979) 6:3073; Cooney *et al.*, Science (1988) 241:456; Dervan *et al.*, Science (1991) 251:1360). These oligomers can be administered *per se* or the relevant oligomers can be expressed *in vivo*. Synthetic antisense or triplex oligonucleotides may comprise modified bases or modified backbones. Examples of the latter include methylphosphonate,  
15 phosphorothioate or peptide nucleic acid backbones. Such backbones are incorporated in the antisense or triplex oligonucleotide in order to provide protection from degradation by nucleases and are well known in the art. Antisense and triplex molecules synthesised with these or other modified backbones also form part of the present invention.

20 In addition, expression of the NOGO polypeptide may be prevented by using ribozymes specific to the NOGO mRNA sequence. Ribozymes are catalytically active RNAs that can be natural or synthetic (see for example Usman, N, et al., Curr. Opin. Struct. Biol (1996) 6(4), 527-33.) Synthetic ribozymes can be designed to specifically cleave NOGO mRNAs at selected  
25 positions thereby preventing translation of the NOGO mRNAs into functional polypeptide. Ribozymes may be synthesised with a natural ribose phosphate backbone and natural bases, as normally found in RNA molecules. Alternatively the ribozymes may be synthesised with non-natural backbones to provide protection from ribonuclease degradation, for example, 2'-O-methyl RNA, and  
30 may contain modified bases.

Preferably the NOGO antagonist is an antibody, more preferably a monoclonal antibody.



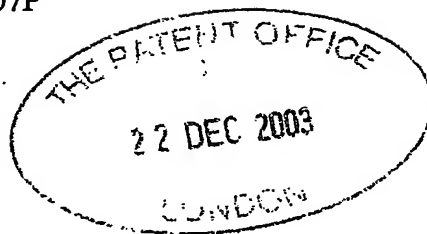
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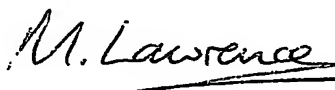
**New Patent Application according to Section 15(1)**  
**Applicants: Glaxo Group Limited**

Herewith are attached the following documents in respect of the above application:

Request for grant (Form 1/77)  
Specification

Could you please acknowledge receipt of this application by returning the enclosed duplicate copy of this letter.

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G M P Lawrence  
Agent for the Applicant

Encs

Preferably the monoclonal antibody is a function-blocking anti-NOGO monoclonal antibody, more preferably a function-blocking anti-NOGO-A monoclonal antibody.

5 Preferably the function-blocking anti-NOGO-A monoclonal antibody comprises CDR's as shown in the tables 1 to 6 which show the CDRs of three independently isolated anti-NOGO antibodies: 2A10/3, 2C4/1 and 15C3/3. The CDR's are identified as described by Kabat (Kabat et al. (1991) "Sequences of proteins of immunological interest"; Fifth Edition; US Department of Health and Human Services; NIH publication No 91-3242). CDRs preferably are as defined  
10 by Kabat but following the principles of protein structure and folding as defined by Chothia and Lesk, (Chothia et al., (1989) "Conformations of immunoglobulin hypervariable regions"; Nature 342, p877-883) it will be appreciated that additional residues may also be considered to be part of the antigen binding region.

15

**Table 1: Antibody 2A10/3 light chain CDRs**

<b>CDR</b>	<b>According to Kabat</b>
L1	RSSKSLLYKDGKTYLN (SEQ ID NO:1)
L2	LMSTRAS (SEQ ID NO:2)
L3	QQLVEYPLT (SEQ ID NO:3)

**Table 2: Antibody 2A10/3 heavy chain CDRs**

20

<b>CDR</b>	<b>According to Kabat</b>
H1	SYWMH (SEQ ID NO:4)
H2	NINPSNGGTNYNEKFKS (SEQ ID NO:5)
H3	GQGY (SEQ ID NO:6)

**Table 3: Antibody 2C4/1 light chain CDRs**

<b>CDR</b>	<b>According to Kabat</b>
------------	---------------------------

L1	RSSQSLVHSNGNTYLH (SEQ ID NO:7)
L2	KVSNRFS (SEQ ID NO:8)
L3	SQSTHVPLT (SEQ ID NO:9)

**Table 4: Antibody 2C4/1 heavy chain CDRs**

<b>CDR</b>	<b>According to Kabat</b>
H1	FSCYAMS (SEQ ID NO:10)
H2	SISDGGSYTYYPDNVKG (SEQ ID NO:11)
H3	ELLFDY (SEQ ID NO:12)

5 **Table 5: Antibody 15C3/3 light chain CDRs**

<b>CDR</b>	<b>According to Kabat</b>
L1	RSSKSLLSNGNTYLY (SEQ ID NO:13)
L2	RMSNLAS (SEQ ID NO:14)
L3	MQHLEYPLT (SEQ ID NO:15)

**Table 6: Antibody 15C3/3 heavy chain CDRs**

<b>CDR</b>	<b>According to Kabat</b>
H1	SYWMN (SEQ ID NO:16)
H2	QIYPGDGDTNYNGKFKG (SEQ ID NO:17)
H3	VRFDY (SEQ ID NO:18)

10

The anti-NOGO antibody may also be an antibody which binds to the same epitope on the NOGO polypeptide as an antibody having the CDRs described above. Preferably the epitope comprises the region 586 to 785 (NOGO-A amino acid numbering). More preferably the epitope is comprised

15 within the region 586 to 685 or 686 to 785. Competitive inhibition assays are used for mapping of the epitopes on an antigen.

The anti-NOGO antibody may be a chimeric antibody which binds to and neutralises NOGO, preferably human NOGO, comprising CDRs such as those disclosed in tables 1 to 6. Preferably the chimeric antibody comprises mouse and human sequences.

5            Preferably the anti-NOGO antibody is a humanised antibody which binds to and neutralises NOGO, preferably human NOGO.

             Preferably the anti-NOGO antibody is an antibody or functional fragment thereof which comprises a heavy chain variable domain which comprises one or more CDR's selected from CDRH1, CDRH2 and CDRH3 of table 1, preferably  
10   comprising at least CDRH3, and/or a light chain variable domain which comprises one or more CDRs selected from CDRL1, CDRL2 and CDRL3 from table 4; an antibody or functional fragment thereof which comprises a heavy chain variable domain which comprises one or more CDR's selected from CDRH1, CDRH2 and CDRH3 of table 2, preferably comprising at least CDRH3,  
15   and/or a light chain variable domain which comprises one or more CDRs selected from CDRL1, CDRL2 and CDRL3 from table 5; or an antibody or functional fragment thereof which comprises a heavy chain variable domain which comprises one or more CDR's selected from CDRH1, CDRH2 and CDRH3 of table 3, preferably comprising at least CDRH3, and/or a light chain variable  
20   domain which comprises one or more CDRs selected from CDRL1, CDRL2 and CDRL3 from table 6.

             More preferably the anti-NOGO antibody or functional fragment thereof comprises:

- 25            a)     a heavy chain variable domain ( $V_H$ ) which comprises in sequence CDRH1, CDRH2 and CDRH3 from table 1,  
             and /or  
             b)     a light chain variable domain ( $V_L$ ) which comprises in sequence CDRL1, CDRL2 and CDRL3 from table 4;

             an anti-NOGO antibody or functional fragment thereof which comprises:

- 30            a)     a heavy chain variable domain ( $V_H$ ) which comprises in sequence CDRH1, CDRH2 and CDRH3 from table 2,  
             and /or

b) a light chain variable domain ( $V_L$ ) which comprises in sequence CDRL1, CDRL2 and CDRL3 from table 5; or

an anti-NOGO antibody or functional fragment thereof which comprises:

5 a) a heavy chain variable domain ( $V_H$ ) which comprises in sequence CDRH1, CDRH2 and CDRH3 from table 3,

and /or

c) a light chain variable domain ( $V_L$ ) which comprises in sequence CDRL1, CDRL2 and CDRL3 from table 6.

10 The anti-NOGO antibody or functional fragment thereof may preferably comprise a heavy chain variable region comprising one of the following amino acid sequences:-

QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGNINPSNGGTN  
YNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCELGGYWGQGTTLTVSS

15 (SEQ ID NO: 37); or

EVQLVESGGGLVKPGGSLKLSCAASGFTFSCYAMSWVRQTPEKRLEWVASISDGGSYTY  
YPDNVKGRFTISRDNKNNLYLQMSHLKSEDTAMYYCAKELLFDYWGQGTTLTVSS

(SEQ ID NO:38); or

20

QVQLQQSGAELVKPGASVKISCKASGYAFSSYWMHWVKQRPGKGLEWIGQIYPGDGDTN  
YNGKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCAVRFDYWGQGTTLTVSS

(SEQ ID NO:39).

25 Further, the anti-NOGO antibody or functional fragment thereof may preferably comprise a heavy chain variable region comprising one of the following amino acid sequences:-

30 DIVITQDELSNPVTSGESVSISSRSSKSLLYKDGTKTYLNWFLQRPQSPQLLIYLMSTR  
ASGVSDRFSGSGSGTDFTLEISRKAEDVGVYYCQQLVEYPLTFGAGTKLELK

(SEQ ID NO:40); or

DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNR  
FSGVPDRFSGSGSGTDFTLKISRVEAEDLGVIYFCQSSTHVPLTFGAGTKLELK  
(SEQ ID NO:41); or

5

DIVMTQAAPSVPTPGESVSISSKSLLSNGNTYLYWFLQRPQSPQLLIYRMSNL  
ASGVPDRFSGSGSGTAFTLRISRVEAEDVGVYYCMQHLEYPLTFGAGTKLELK  
(SEQ ID NO:42).

- 10 The boxed sequences in SEQ ID Nos 37 to 42 represent the CDR sequences according to Kabat et al *supra*.

In a preferred embodiment the anti-NOGO antibody comprises:

- a) a heavy chain variable region of SEQ ID NO:37 together with a light chain variable region comprising the amino acid sequence of SEQ ID NO:40; or  
15 b) a heavy chain variable region of SEQ ID NO:38 together with a light chain variable region comprising the amino acid sequence of SEQ ID NO:41; or  
c) a heavy chain variable region of SEQ ID NO:39 together with a light chain variable region comprising the amino acid sequence of SEQ ID NO:42.

- 20 More preferably the anti-NOGO antibody, or functional fragment thereof, comprises either:

- a heavy chain variable fragment comprising SEQ ID NO:37 and a constant part or fragment thereof of a human heavy chain; and  
a light chain variable fragment comprising SEQ ID No:40 and a constant part or fragment thereof of a human light chain; or  
25 a heavy chain variable fragment comprising SEQ ID NO:38 and a constant part or fragment thereof of a human heavy chain; and  
a light chain variable fragment comprising SEQ ID No:41 and a constant part or fragment thereof of a human light chain; or  
a heavy chain variable fragment comprising SEQ ID NO:39 and a constant part  
30 or fragment thereof of a human heavy chain; and  
a light chain variable fragment comprising SEQ ID No:42 and a constant part or fragment thereof of a human light chain.

Still more preferably the anti-NOGO antibody is selected from 2A10/3, 2C4/1 or 15C3/3, preferably the humanised form thereof. Most preferably the anti-NOGO antibody is 2A10/3 or the humanised form thereof.

Anti-NOGO antibody 2A10/3 comprises a heavy chain variable region  
5 having the amino acid sequence of SEQ ID NO:37 and a light chain variable region having the amino acid sequence of SEQ ID NO:40.

Anti-NOGO antibody 2C4/1 comprises a heavy chain variable region having the amino acid sequence of SEQ ID NO:38 and a light chain variable region having the amino acid sequence of SEQ ID NO:41.

10 Anti-NOGO antibody 15C3/3 comprises a heavy chain variable region having the amino acid sequence of SEQ ID NO:39 and a light chain variable region having the amino acid sequence of SEQ ID NO:42.

The anti-NOGO antibody may be prepared using standard methods. In particular the NOGO antibody may be prepared using polynucleotides as  
15 described below. For example preferred polynucleotides encoding CDRH1, CDRH2, CDRH3, CDRL1, CDRL2 and CDRL3, as disclosed in tables 1 to 6, are shown below in tables 7 to 12.

**Table 7: Antibody 2A10/3 light chain CDRs**

20

CDR	
L1	AGGTCTAGTAAGAGTCTCCTATATAAGGATG GGAAGACATACTTGAAT (SEQ ID NO:19)
L2	TTGATGTCCACCCGTGCATCA (SEQ ID NO:20)
L3	CAACAACCTTGTAGAGTATCCGCTCACG (SEQ ID NO:21)

**Table 8: Antibody 2A10/3 heavy chain CDRs**

CDR	
H1	AGCTACTGGATGCAC (SEQ ID NO:22)

H2	AATATTAATCCTAGCAATGGTGGTACTAACTACAAT GAGAAGTTCAAGAGC (SEQ ID NO:23)
H3	GGACAGGGCTAC (SEQ ID NO:24)

**Table 9: Antibody 2C4/1 light chain CDRs**

CDR	
L1	AGATCTAGTCAGAGCCTTGTACACAGTAATG GAAACACCTATTTACAT (SEQ ID NO:25)
L2	AAAGTTTCCAACCGATTTTCT (SEQ ID NO:26)
L3	TCTCAGAGTACACATGTTCCG CTCACG (SEQ ID NO:27)

**5 Table 10: Antibody 2C4/1 heavy chain CDRs**

CDR	
H1	TTCAGTTGCTATGCCATGTCT (SEQ ID NO:28)
H2	TCCATTAGTGATGGTGGTAGTTACACCTACTATCCA GACAATGTAAAGGGC (SEQ ID NO:29)
H3	GAACTACTTTTGGACTAC (SEQ ID NO:30)

**Table 11: Antibody 15C3/3 light chain CDRs**

CDR	
L1	AGGTCTAGTAAGAGTCTCCTGCATAGTAATGGCAA CACTTACTTGTAT (SEQ ID NO:31)
L2	CGGATGTCCAACCTTGCCTCA (SEQ ID NO:32)
L3	ATGCAACATCTAGAATATCCGCTCACG (SEQ ID NO:33)

10

**Table 12: Antibody 15C3/3 heavy chain CDRs**



<b>CDR</b>	
H1	AGCTACTGGATGAAC (SEQ ID NO:34)
H2	CAGATTTATCCTGGAGATGGTGATACTAACTACAAC GGAAAGTTCAAGGGC (SEQ ID NO:35)
H3	GTACGCTTTGACTAT (SEQ ID NO:36)

Further, preferred polynucleotides encoding the heavy chain variable region comprising the amino acid sequences of SEQ ID NOs 37 to 39 and light chain variable regions comprising the amino acid sequences of SEQ ID NOs 40 to 42 are shown below.

A preferred polynucleotide sequence encoding the amino acid sequence of SEQ ID NO:37 is

CCAGGTCCAAC TGCAGCAGCCTGGGACTGAACTGGTGAAGCCTGGGGCTTCAGTGAAGC  
10 TGTCTTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCACTGGGTGAAGCAG  
AGGCCTGGACAAGGCCTTGAGTGGATTGGAAATATTAATCCTAGCAATGGTGGTACTAA  
CTACAATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAG  
CCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTATTGTGAACTG  
GGACAGGGCTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA  
15 (SEQ ID NO:43)

A preferred polynucleotide sequence encoding the amino acid sequence of SEQ ID NO:38 is:

GAAGTGCAGCTGGTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGGAGGGTC  
20 CCTGAAACTCTCCTGTGCAGCCTCTGGATTCACTTTTCACTTGCTATGCCA  
TGTCTTGGGTTCCGAGACTCCGGAAAAGAGGCTGGAGTGGGTTCGCATCC  
ATTAGTGATGGTGGTAGTTACACCTACTATCCAGACAATGTAAAGGGCCG  
ATTCACCATCTCCAGAGACAATGCCAAGAACAACCTGTACCTGCAAATGA  
GCCATCTGAAGTCTGAGGACACAGCCATGTATTACTGTGCAAAGGAATA  
25 CTTTTTGA CTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA  
(SEQ ID NO:44)

A preferred polynucleotide sequence encoding the amino acid sequence of SEQ ID NO:39 is:

CAGGTTCACTGCAGCAGTCTGGGGCTGAGCTGGTGAAGCCTGGGGCCTC  
30 AGTGAAGATTTCTTGCAAAGCTTCTGGCTACGCATTCAGTAGCTACTGGA  
TGAAGTGGGTGAAGCAGAGGCCTGGAAAGGGTCTTGAGTGGATTGGACAG

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ATTTATCCTGGAGATGGTGATACTAACTACAACGGAAAGTTCAAGGGCAA  
GGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACATGCAGCTCA  
GCAGCCTGACCTCTGAGGACTCTGCGGTCTATTTCTGTGCAGTACGCTTT  
GACTATTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA  
5 (SEQ ID NO:45)

A preferred polynucleotide sequence encoding the amino acid sequence of SEQ  
ID NO:40 is:

10 GATATTGTGATAACCCAGGATGAACTCTCCAATCCTGTCACTTCTGGAGA  
ATCAGTTTCCATCTCCTGCAGGTCTAGTAAGAGTCTCCTATATAAGGATG  
GGAAGACATACTTGAATTGGTTTCTGCAGAGACCAGGACAATCTCCTCAG  
CTCCTGATCTATTTGATGTCCACCCGTGCATCAGGAGTCTCAGACCGGTT  
TAGTGGCAGTGGGTGAGAACAGATTTTACCCTGGAAATCAGTAGAGTGA  
15 AGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACCTGTAGAGTATCCG  
CTCACGTTCCGGTGCTGGGACCAAGCTGGAGCTGAAA  
(SEQ ID NO:46)

A preferred polynucleotide sequence encoding the amino acid sequence of SEQ  
20 ID NO:41 is:

GATGTTGTGATGACCCAAACTCCACTCTCCCTGCCTGTGAGTCTTGGAGA  
TCAAGCCTCCATCTCTTGCAGATCTAGTCAGAGCCTTGTACACAGTAATG  
GAAACACCTATTTACATTGGTACCTGCAGAAGCCAGGCCAGTCTCCAAAG  
25 CTCCTGATCTACAAAGTTTCCAACCGATTTTCTGGGGTCCCAGACAGGTT  
CAGTGGCAGTGGATCAGGGACAGATTTTCACTCAAGATCAGCAGAGTGG  
AGGCTGAGGATCTGGGAGTTTATTCTGCTCTCAGAGTACACATGTTCCG  
CTCACGTTCCGGTGCTGGGACCAAGCTGGAGCTGAAA  
(SEQ ID NO:47)

30 A preferred polynucleotide sequence encoding the amino acid sequence of SEQ  
ID NO:42 is:

GATATTGTGATGACTCAGGCTGCACCCTCTGTACCTGTCACTCCTGGAGA  
35 GTCAGTATCCATCTCCTGCAGGTCTAGTAAGAGTCTCCTGCATAGTAATG  
GCAACACTTACTTGTATTGGTTCCTGCAGAGGCCAGGCCAGTCTCCTCAG  
CTCCTGATATATCGGATGTCCAACCTTGCCTCAGGAGTCCCAGACAGGTT  
CAGTGGCAGTGGGTGAGAACTGCTTTTCACTGAGAATCAGTAGAGTGG  
AGGCTGAGGATGTGGGTGTTTATTACTGTATGCAACATCTAGAATATCCG  
40 CTCACGTTCCGGTGCTGGGACCAAGCTGGAGCTGAAA

(SEQ ID NO:48)

The method of the invention may be carried out *in-vitro* or *in-vivo*. When carried out *in-vitro* the method may be a model for amyloid deposition, APP  
5 processing, or BACE activity or it may provide a means to screen for compounds useful in the treatment of neurological diseases such as Alzheimer's disease.

When carried out *in-vivo* the method of the invention may be a method of prophylaxis or treatment of neurological diseases/disorders including, but not limited to, acute diseases such as stroke, traumatic brain injury and spinal cord  
10 injury as well as chronic diseases including Alzheimer's disease, fronto-temporal dementias (tauopathies), peripheral neuropathy, Parkinson's disease, Huntington's disease, Creutzfeldt-Jakob Disease (CJD), multiple sclerosis and inclusion body myositis.

In a preferred embodiment the method is a method of prophylaxis or  
15 treatment of neurological disease that is involving amyloidosis. In a more preferred embodiment the amyloidosis is precipitated by an amyloidogenic peptide derived from APP, preferably A $\beta$ ; that is A $\beta$ 40, A $\beta$ 42 or both A $\beta$ 40 and A $\beta$ 42. Still more preferably the invention relates to a method of prophylaxis or treatment of Alzheimer's disease, fronto-temporal dementias (tauopathies),  
20 peripheral neuropathy, Parkinson's disease, Huntington's disease, Creutzfeldt-Jakob Disease (CJD), multiple sclerosis or inclusion body myositis. Most preferably the invention relates to a method of prophylaxis or treatment of Alzheimer's disease.

The method of prophylaxis or treatment comprises the use of a  
25 therapeutic agent or pharmaceutical composition in the treatment of the disease as described hereinbelow.

In another aspect the invention provides the use of a NOGO antagonist in the manufacture of a medicament for the prophylaxis or treatment of neurological diseases/disorders including, but not limited to, acute diseases such as stroke,  
30 traumatic brain injury and spinal cord injury as well as chronic diseases including Alzheimer's disease, fronto-temporal dementias (tauopathies), peripheral neuropathy, Parkinson's disease, Huntington's disease, Creutzfeldt-Jakob Disease (CJD), multiple sclerosis and inclusion body myositis.

In a preferred embodiment the invention provides the use of NOGO antagonist for the manufacture of a medicament for the prophylaxis or treatment of a neurological disease that is involving amyloidosis. In a more preferred embodiment the amyloidosis is precipitated by an amyloidogenic peptide derived from APP, preferably A $\beta$ ; that is A $\beta$ 40, A $\beta$ 42 or both A $\beta$ 40 and A $\beta$ 42. Still more preferably the invention relates to the use of a NOGO antagonist for the manufacture of a medicament for the prophylaxis or treatment of Alzheimer's disease, fronto-temporal dementias (tauopathies), peripheral neuropathy, Parkinson's disease, Huntington's disease, Creutzfeldt-Jakob Disease (CJD), multiple sclerosis or inclusion body myositis. Most preferably the invention relates to the use of a NOGO antagonist for the manufacture of a medicament for the prophylaxis or treatment of Alzheimer's disease.

The NOGO antagonist for use in the method of the invention, including the method of treatment or the use for the manufacture of a medicament as hereinabove defined, is preferably a NOGO-A antagonist, most preferably a monoclonal antibody.

Preferably the monoclonal antibody is a function-blocking anti-NOGO-A antibody as described hereinabove. An example of such a preferred function-blocking anti-NOGO-A antibody is 2A10/3 as described hereinabove, or most preferably a humanised version thereof. Other examples are 2C4/1 and 15C3/3 or humanised versions thereof.

The NOGO antagonist may be administered as a prophylactic or post injury, or as otherwise needed. The dose and duration of treatment relates to the relative duration of the molecules of the present invention in the human circulation, and can be adjusted by one of skill in the art depending upon the condition being treated and the general health of the patient.

The mode of administration of the NOGO antagonist may be any suitable route which delivers the agent to the host. The NOGO antagonists and pharmaceutical compositions thereof are particularly useful for parenteral administration, i.e., subcutaneously, intrathecally, intraperitoneally, intramuscularly, intravenously, or intranasally.

NOGO antagonists may be prepared as pharmaceutical compositions containing an effective amount of the NOGO antagonist as an active ingredient in

a pharmaceutically acceptable carrier. In the prophylactic agent of the invention, an aqueous suspension or solution containing the antagonist, preferably buffered at physiological pH, in a form ready for injection is preferred. The compositions for parenteral administration will commonly comprise a solution of the antagonist  
5 or a cocktail thereof dissolved in an pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers may be employed, e.g., 0.9% saline, 0.3% glycine, and the like. These solutions are sterile and generally free of particulate matter. These solutions may be sterilized by conventional, well known sterilization techniques (e.g., filtration). The  
10 compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, etc. The concentration of the antagonist in such pharmaceutical formulation can vary widely, i.e., from less than about 0.5%, usually at or at least about 1% to as much as 15 or 20% by weight and will be  
15 selected primarily based on fluid volumes, viscosities, etc., according to the particular mode of administration selected.

Thus, a pharmaceutical composition for intramuscular injection could be prepared to contain 1 mL sterile buffered water, and between about 1 ng to about 100 mg, e.g. about 50 ng to about 30 mg or more preferably, about 5 mg to about  
20 25 mg, of a NOGO antagonist. Similarly, a pharmaceutical composition of the invention for intravenous infusion could be made up to contain about 250 ml of sterile Ringer's solution, and about 1 to about 30 and preferably 5 mg to about 25 mg of an antagonist. Actual methods for preparing parenterally administrable compositions are well known or will be apparent to those skilled in the art and are  
25 described in more detail in, for example, Remington's Pharmaceutical Science, 15th ed., Mack Publishing Company, Easton, Pennsylvania.

It is preferred that the NOGO antagonist, when in a pharmaceutical preparation, be present in unit dose forms. The appropriate therapeutically effective dose can be determined readily by those of skill in the art. To effectively  
30 treat neurological diseases in a human, one dose of up to 700 mg per 70 kg body weight of an antagonist should be administered parenterally, preferably *i.v.* or *i.m.* (intramuscularly). Such dose may, if necessary, be repeated at appropriate time intervals selected as appropriate by a physician.

The NOGO antagonists described herein can be lyophilized for storage and reconstituted in a suitable carrier prior to use. Where the NOGO antagonist is an antibody this technique has been shown to be effective with conventional immunoglobulins and art-known lyophilization and reconstitution techniques can be employed.

The following examples illustrate the invention.

### Examples

#### Example 1 – Transfection of NOGO A cDNA into SHSY5Y-APP cells

- 10 The day before transfection the SHSY5Y-APPwt cells were trypsinised, counted and replated at 1million cells per well of a 6-well plate (Nunc).  
The NOGO expression construct (FLAG-tagged NOGO-A cDNA in pCDNA3 (Invitrogen); MYC-tagged NOGO-B and NOGO-C in pCDNA3.1A) was complexed with Plus<sup>TM</sup> reagent by diluting the DNA into serum free medium  
15 (OptiMEM-1), adding Plus<sup>TM</sup> reagent, mixing and incubating at room temperature for 15 min. (6ul Plus reagent into a total volume of 100ul with 2ug DNA and OptiMEM-1 per well)  
LipofectAMINE<sup>TM</sup> reagent was diluted into serum free medium (Optimem-I) in a second tube and mixed (4ul Lipofectamine in 100ul volume per well).  
20 Pre-complexed DNA (from above) was combined with the diluted lipofectAMINE, mixed and incubated at room temp for 15 min.  
Meanwhile the cells were washed with serum free medium (OptiMEM-I) and then fresh serum free medium was added to the cells (800ul per well).  
The DNA-Plus-LipofectAMINE reagent complexes were then added to the cells  
25 (200ul), mixed gently and the cells incubated at 37oC for 5hr in 5% CO2.  
After 5 hours 1ml serum containing growth medium was added to the cells and the cells incubated overnight or 2hours.  
After 14 hours (or 2 hours) all medium was removed and replaced with 1ml (OptiMEM-1) per well.  
30 After 48 hours medium conditioning the medium was collected and assayed for amyloid content as described in example 2.

#### Example 2 – Detection of A $\beta$ peptide by IGEN ELISA

SHSY5Y cells overexpressing the human APPwt or Amyloid Precursor Protein Swedish variant sequence (APPswe) were seeded in 96 well Nunc plates at a density of  $1 \times 10^5$  cells/well.

After 24 hours the reagents (eg. antibody, peptides, compounds etc) for testing were added to the cells in a final volume of 120 $\mu$ l and cells incubated for 24hr.

The medium was removed from cells and 50 $\mu$ l was assayed for A $\beta$  x-40 and 50 $\mu$ l for A $\beta$  x-42 in an overnight ORIGEN immunoassay employing A $\beta$  C-terminal specific antibodies. Briefly, A $\beta$  peptides were captured using biotinylated 6E10 (Signet Labs). Ori-tagged labelled A $\beta$  C-terminal specific antibodies were used to detect the A $\beta$  x-40 and A $\beta$  x-42 species. Antibody- A $\beta$  complexes were captured with streptavidin coated dynabeads and assayed in an IGEN M8 analyser.

The viability of the cells was checked using MTT (3-[4,5-Dimethylthiazol-2-yl]-2,5-diphenyltetrazolium bromide; Thiazolyl blue) reagent. Briefly, MTT reagent (5mg/ml in phosphate buffered saline) was diluted 1:10 in culture medium and 100 $\mu$ l added to each well. Following incubation at 37°C for 4hr, 100 $\mu$ l solubilising solution (20% SDS/50% Dimethyl Formamide) was added. Absorbance of plates was read using a Delfia Wallac plate reader at 590nm.

The results are shown in figures 1 to 14.

SHSY5Y-APPwt cells express wild-type APP. SHSY5Y-APPswe cells express the Swedish mutation form of APP.

### **Example 3 - The effect of NOGO-A expression on levels of secreted A $\beta$ 40 and A $\beta$ 42 peptide**

When an expression construct expressing NOGO-A is introduced into either SHSY5Y-APPwt cells or SHSY5Y-APPswe cells the levels of A $\beta$  40 and A $\beta$  42 are seen to significantly increase suggesting that NOGO-A is in some way modulating, directly or indirectly, the proteolytic processing of APP and/ or degradation of A $\beta$  peptides. The fact that the product of this altered APP processing is the peptide A $\beta$ 40 could suggest that the effect of NOGO could be at the level of modulating  $\beta$ -secretase activity.

Figure 1 shows the increase in the level of secreted A $\beta$ 40 when NOGO-A is expressed from an expression vector. The two left-hand bars are the controls (vector alone and vector carrying a control protein, green fluorescent protein (GFP)), showing the background levels of A $\beta$ 40 production in this cell-line. The remaining bars show that significantly increased level of A $\beta$ 40 peptide are detected when NOGO-A, fused to a FLAG peptide, is expressed in the cells and also that a similar elevation, albeit less marked, when NOGO-B, fused to myc, is expressed.

The same experiment was repeated using an ELISA specific for A $\beta$ 42. The results showed a similar elevation in levels of A $\beta$  42 peptide secretion as that seen in the earlier experiment using A $\beta$  40 ELISA. Again NOGO-B also showed increased secretion of A $\beta$  42 peptide and again the increase was less marked than with NOGO-A. The results are shown in figure 2.

Repeat experiments comparing levels of secreted peptide from cells transfected with NOGO-A compared to vector pCDNA3 alone, are shown in figures 3 (for A $\beta$  40) and 4 (for A $\beta$  42).

A direct comparison of levels of A $\beta$  40 and A $\beta$  42 peptide secreted is shown in figure 5.

#### **Example 4 – Preparation of an anti-NOGO antibodies.**

##### Preparation and selection of the hybridomas

Anti-NOGO monoclonal antibodies are produced by hybridoma cells, the result of the fusion of mouse myeloma cells with B lymphocytes from mice immunised with the target antigen. The hybridoma cell is immortalised by the myeloma fusion partner while the capacity to produce antibodies is provided by the B lymphocyte. Each hybridoma cell makes only one individual antibody with unique specificity hence the term monoclonal.

SJL mice were immunised with 10 $\mu$ g total protein (1:1, human NOGO-A splice (amino acids 186-1004) and rat NOGO-A splice (amino acids 173-975), produced as GST-fusion proteins in E coli BL21) using both CFA and RIBI adjuvants subcutaneously. The mice were then boosted with 5 $\mu$ g of the same proteins using RIBI adjuvant after 4 and 8 days. After a further 3 days, immune cells were harvested from the locally draining lymph nodes and fused with mouse



myeloma cells using PEG1500 to generate hybridomas. Individual hybridoma cell lines were cloned by two rounds of limiting dilution.

Initial hybridoma antibody selection was on the basis of direct binding to the NOGO protein(s) on microtitre plates. Subsequently ca. 60 hybridomas were  
5 selected based on the ability of soluble protein (consisting of human Nogo-A sequence cleaved from the GST moiety using Precision protease) to compete for this binding activity in ELISA assays.

Cloning of the variable regions

Total RNA was extracted from the selected 2A10/3, 2C4/1 and 15C3/3  
10 hybridoma cells followed by reverse transcription and polymerase chain reaction (RT-PCR) to extract heavy and light variable-domain cDNA sequence. The forward primer for RT-PCR was a mixture of degenerate primers specific for murine immunoglobulin gene leader-sequences and the reverse primer was an isotype-specific antibody directed to the constant regions. PCR primers were  
15 designed to carry 5' restriction enzyme recognition sites to enable cloning into pUC19 for DNA sequencing.

RNA extraction

Total RNA was extracted from pellets of  $10^6$  cells of each hybridoma clone using the SV Total RNA Isolation System from Promega according to manufacturer's  
20 instructions.

Reverse transcription

RNA was reverse transcribed to produce cDNA of the variable heavy and light domains using forward primers specific for the murine leader sequences and reverse primers to murine IgG $\kappa$  constant regions. The IgG $\gamma$ 1 reverse primer was  
25 used for hybridomas 2C4/1 and 15C3/3; and the IgG $\gamma$ 2b for 2A10/3. Forward primers carry a Sall restriction enzyme recognition site at the 5' end, with four extra nucleotides added 5' to this for efficient restriction digestion. These primers were adapted from Jones ST and Bendig MM 1991 (Biotechnology 9, 88-89). Reverse primers carry a XmaI restriction enzyme recognition site plus and  
30 extra four nucleotides at the 5' ends.

Primers:

Murine V<sub>H</sub> leader sequence forward primers:

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AG77: 5'-ACT AGT CGA CAT GAA ATG CAG CTG GGT CAT STT CTT  
C-3'

AG78: 5'-ACT AGT CGA CAT GGG ATG GAG CTR TAT CAT SYT CTT-  
3'

5 AG79: 5'-ACT AGT CGA CAT GAA GWT GTG GTT AAA CTG GGT TTT  
T-3'

AG80: 5'-ACT AGT CGA CAT GRA CTT TGG GYT CAG CTT GRT TT-3'

AG81: 5'-ACT AGT CGA CAT GGA CTC CAG GCT CAA TTT AGT TTT  
CCT T-3'

10 AG82: 5'-ACT AGT CGA CAT GGC TGT CYT RGS GCT RCT CTT CTG  
C-3'

AG83: 5'-ACT AGT CGA CAT GGR ATG GAG CKG GRT CTT TMT CTT-  
3'

AG84: 5'-ACT AGT CGA CAT GAG AGT GCT GAT TCT TTT GTG-3'

15 AG85: 5'-ACT AGT CGA CAT GGM TTG GGT GTG GAM CTT GCT ATT  
CCT G-3'

AG86: 5'-ACT AGT CGA CAT GGG CAG ACT TAC ATT CTC ATT CCT  
G-3'

AG87: 5'-ACT AGT CGA CAT GGA TTT TGG GCT GAT TTT TTT TAT  
20 TG-3'

AG89: 5'-ACT AGT CGA CAT GAT GGT GTT AAG TCT TCT GTA CCT  
G-3'

Murine  $V_L$  leader sequence forward primers:

25 AG90: 5'-ACT AGT CGA CAT GAA GTT GCC TGT TAG GCT GTT GGT  
GCT G-3'

AG91: 5'-ACT AGT CGA CAT GGA GWC AGA CAC ACT CCT GYT ATG  
GGT-3'

AG92: 5'-ACT AGT CGA CAT GAG TGT GCT CAC TCA GGT CCT GGC GTT  
30 G-3'

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AG93: 5'-ACT AGT CGA CAT GAG GRC CCC TGC TCA GWT TYT TGG  
MWT CTT G-3'

AG94: 5'-ACT AGT CGA CAT GGA TTT WCA GGT GCA GAT TWT CAG  
CTT C-3'

5 AG95: 5'-ACT AGT CGA CAT GAG GTK CYY TGY TSA GYT YCT GRG  
G-3'

AG96: 5'-ACT AGT CGA CAT GGG CWT CAA GAT GGA GTC ACA KWW  
YCW GG-3'

10 AG97: 5'-ACT AGT CGA CAT GTG GGG AYC TKT TTY CMM TTT TTC  
AAT TG-3'

AG98: 5'-ACT AGT CGA CAT GGT RTC CWC ASC TCA GTT CCT TG-3'

AG99: 5'-ACT AGT CGA CAT GTA TAT ATG TTT GTT GTC TAT TTC T-  
3'

15 AG100: 5'-ACT AGT CGA CAT GGA AGC CCC AGC TCA GCT TCT CTT  
CC-3'

MKV12: 5'-ACT AGT CGA CAT GAA GTT TCC TTC TCA ACT TCT GCT  
C-3'

Murine  $\gamma$ 1 constant region reverse primer:

20 AG102: 5'-GGA TCC CGG GCC AGT GGA TAG ACA GAT G-3'

Murine  $\gamma$ 2b constant region reverse primer:

AG104: 5'-GGA TCC CGG GAG TGG ATA GAC TGA TGG-3'

25 Murine  $\kappa$  constant region reverse primer:

AG101: 5'-GGA TCC CGG GTG GAT GGT GGG AAG ATG-3'

Pools of murine  $V_H$  or  $V_L$  leader sequence forward primers were prepared at  
50 $\mu$ M. Solutions of the murine  $\gamma$  or  $\kappa$  constant region reverse primers were also

30 prepared at 50 $\mu$ M.

**RT-PCR**

Reverse transcription of the RNA encoding the variable heavy and light regions was carried out in duplicate using the Access RT-PCR System from Promega according to manufacturer's instructions. Approximately 200ng RNA was  
5 included in a 50 µl reaction containing RT-PCR buffer supplied, 0.2 mM dNTPs, 1uM of each primer set, 1uM MgSO<sub>4</sub> and 5U each of AMV Reverse transcriptase and Tfl DNA polymerase.

RT-PCR cycle:

- 1- 48°C for 45min
- 2- 94°C for 2min
- 10 3- 94°C for 30sec
- 4- 50°C for 1min
- 5- 68°C for 2min
- 6- 68°C for 7min

steps 3 to 5: repeat 30 times.

15

**pUC19 cloning**

The variable region RT-PCR products were purified using a Qiagen MinElute Qiagen PCR Purification kit according to their instructions and digested sequentially with XmaI and Sall from New England Biolabs according to  
20 manufacturer's instructions. They were then loaded on a preparative 1% agarose gel containing 0.5% ethidium bromide and run in TAE buffer at 50mA for 1hour and the V region bands excised under ultra-violet light. The DNA fragments were purified from the gel using the MinElute Gel extraction kit from Qiagen according to manufacturer's instructions. pUC19 vector arms were prepared by digesting  
25 pUC19 with Sall and XmaI, then purified using the MinElute Reaction Clean up kit from Qiagen and dephosphorylated using Shrimp alkaline phosphatase (USB) according to the manufacturer's instructions. The concentration of the vector arms and the V-region fragments was estimated from an analytical 1% agarose/ethidium bromide gel, mixed in a molar ratio of 1:2 and ligated using  
30 Promega's Quick Ligation kit according to the manufacturer's instructions. Ligated plasmids were transformed into DH5a cells (Invitrogen) according to manufacturer's instructions. Colonies which grew on L-agar plates containing 100ug/ml ampicillin were selected for DNA sequence analysis.

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### Variable region sequencing

Colonies were cultured overnight at 37°C in 5ml LB medium supplemented with 100µg/ml ampicillin and plasmid DNA was extracted and purified using the Qiagen QIAprep Spin Miniprep kit according to manufacturer's instructions. The

- 5 V<sub>H</sub> and V<sub>L</sub> regions were DNA sequenced using standard M13 forward and reverse primers.

The results of the sequencing determination are shown as SEQ ID NOs 43 to 48.

### Heavy chain variable regions:

#### 2A10/3

- 10 CCAGGTCCAAGTGCAGCAGCCTGGGACTGAACTGGTGAAGCCTGGGGCTTCAGTG  
AAGCTGTCTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCACTGGG  
TGAAGCAGAGGCCTGGACAAGGCTTGAGTGGATTGGAAATATTAATCCTAGCAA  
TGGTGGTACTAACTACAATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGAC  
AAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTG  
15 CGGTCTATTATTGTGAAGTGGGACAGGGCTACTGGGGCCAAGGCACCACTCTCAC  
AGTCTCCTCA  
(SEQ ID NO:43)

- 20 QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPQGLEWIGNINPS  
NGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCELGQGYWGQGT  
LTVSS  
(SEQ ID NO: 37)

#### 2C4/1

- 25 GAAGTGCAGCTGGTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGGAGGGTC  
CCTGAAACTCTCCTGTGCAGCCTCTGGATTCACTTTCAGTTGCTATGCCA  
TGTCTTGGGTTCGCCAGACTCCGAAAAGAGGCTGGAGTGGGTTCGCATCC  
ATTAGTGATGGTGGTAGTTACACCTACTATCCAGACAATGTAAAGGGCCG  
ATTCACCATCTCCAGAGACAATGCCAAGAACAACCTGTACCTGCAAATGA  
30 GCCATCTGAAGTCTGAGGACACAGCCATGTATTACTGTGCAAAGGAACTA  
CTTTTGTACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA  
(SEQ ID NO:44)

- 35 EVQLVESGGGLVKPGGSLKLSAASGFTFSCYAMSWVRQTPEKRLEWVASISDG  
GSYTYYPDNVKGRTISRDNANKNNLYLQMSHLKSEDTAMYYCAKIELLFDYWGQG  
TTLTVSS  
(SEQ ID NO:38)

15C3/3

CAGGTTTCAGCTGCAGCAGTCTGGGGCTGAGCTGGTGAAGCCTGGGGCCTC  
 AGTGAAGATTTCTGCAAAGCTTCTGGCTACGCATTCAGTAGCTACTGGA  
 5 TGAAGTGGGTGAAGCAGAGGCCTGGAAAGGGTCTTGAGTGGATTGGACAG  
 ATTTATCCTGGAGATGGTGATACTAACTACAACGGAAAGTTCAAGGGCAA  
 GGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACATGCAGCTCA  
 GCAGCCTGACCTCTGAGGACTCTGCGGTCTATTTCTGTGCAGTACGCTTT  
 GACTATTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA  
 10 (SEQ ID NO:45)

QVQLQQSGAELVKPGASVKISCKASGYAFS[SYWMN]WVKQRPKGLEWIG[QIYPG]  
 [DGD]TNYNGKFKG[KAT]LTADKSSSTAYMQLSSLTSEDSAVYFCA[VRFDY]WGQGT  
 LTVSS  
 15 (SEQ ID NO:39)

Light chain variable regions:

2A10/3

GATATTGTGATAACCCAGGATGAACTCTCCAATCCTGTCACCTTCTGGAGA  
 20 ATCAGTTTCCATCTCCTGCAGGTCTAGTAAGAGTCTCCTATATAAGGATG  
 GGAAGACATACTTGAATTGGTTTCTGCAGAGACCAGGACAATCTCCTCAG  
 CTCCTGATCTATTTGATGTCCACCCGTGCATCAGGAGTCTCAGACCGGTT  
 TAGTGGCAGTGGGTCAGGAACAGATTTACCCCTGGAAATCAGTAGAGTGA  
 AGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACCTTGTAAGATATCCG  
 25 CTCACGTTTCGGTGCTGGGACCAAGCTGGAGCTGAAA  
 (SEQ ID NO:46)

DIVITQDELSNPVTSGESVSI[SC]R[SSKSLLYKD]GKTYLN[WFLQ]RPGQSPQLLIY  
 [LMSTRAS]GVSDRFSGSGSGTDFTLEISR[KAEDV]GVYYC[QQLVEYPLT]FGAGTK  
 30 LELK  
 (SEQ ID NO:40)

2C4/1

GATGTTGTGATGACCCAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGA  
 35 TCAAGCCTCCATCTCTTGCAGATCTAGTCAGAGCCTTGTAACACAGTAATG  
 GAAACACCTATTTACATTGGTACCTGCAGAAGCCAGGCCAGTCTCCAAAG  
 CTCCTGATCTACAAAGTTTCCAACCGATTTTCTGGGGTCCCAGACAGGTT  
 CAGTGGCAGTGGATCAGGGACAGATTTCACTCAAGATCAGCAGAGTGG

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AGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAGAGTACACATGTTCCG  
CTCACGTTTCGGTGCTGGGACCAAGCTGGAGCTGAAA  
(SEQ ID NO:47)

5 DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIY  
KVSNRFS GVPDRFSGSGSGTDFTLKISRVEAEDLGVYFC SQSTHYPLTFGAGTK  
LELK  
(SEQ ID NO:41)

10 15C3/3  
GATATTGTGATGACTCAGGCTGCACCCTCTGTACCTGTCACCTCCTGGAGA  
GTCAGTATCCATCTCCTGCAGGTCTAGTAAGAGTCTCCTGCATAGTAATG  
GCAACACTTACTTGTATTGGTTCCTGCAGAGGCCAGGCCAGTCTCCTCAG  
CTCCTGATATATCGGATGTCCAACCTTGCCTCAGGAGTCCCAGACAGGTT  
15 CAGTGGCAGTGGGTCAGGAAGTCTTTCACACTGAGAATCAGTAGAGTGG  
AGGCTGAGGATGTGGGTGTTTATTACTGTATGCAACATCTAGAATATCCG  
CTCACGTTTCGGTGCTGGGACCAAGCTGGAGCTGAAA  
(SEQ ID NO:48)

20 DIVMTQAAPSVPVTPGESVSISSRSSKSLLSNGNTYLYWFLQRPQGSPQLLIY  
RMSNLAS GVPDRFSGSGSGTAFTLRISRVEAEDVGVYYCMQHLEYPLTFGAGTK  
LELK  
(SEQ ID NO:42).

25 The DNA sequences for the light or heavy chain regions are given for the  
antibodies 2A10/3, 2C4/1 and 15C3/3. Below each DNA sequence is the  
predicted amino acid sequence encoded by that DNA and the CDRs are shown  
in boxes.

### Recombinant anti-NOGO antibodies

30 Recombinant antibodies having murine 2a/k constant regions could be purified  
from cells transfected with plasmids comprising the light and heavy variable  
regions cloned onto mouse IgG2a/k constant region gene segments. The cloned  
murine V regions were amplified by PCR to introduce restriction sites required for  
cloning into mammalian expression vectors Rld and Rln. Hind III and Spe I sites  
35 were designed in frame with the V<sub>H</sub> domain to allow cloning into a modified Rld  
vector containing the mouse  $\gamma$ 2a constant region. Hind III and BsiW I sites were

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designed in frame the V<sub>L</sub> domain and allow cloning into a modified Rln vector containing the mouse  $\kappa$  constant region.

### PCR primers

2A10 V<sub>H</sub> forward primer:

5 5'-  
ACTCATAAGCTTGCCACCATGGGATGGAGCTGTATCATCCTCTTTTGGTAG  
-3'

V<sub>H</sub> reverse primer:

5'-ACTATGACTAGTGTGCCTTGGCCCCAGTAG-3'

10 V<sub>L</sub> forward primer:

5'- ACTCATAAGCTTGCCACCATGAGGTGCTCTCTTCAGTTTCTG -3'

V<sub>L</sub> reverse primer:

5'- ACTATGCGTACGTTTCAGCTCCAGCTTGG -3'

15 PCR was performed using Hercules (Stratagene) according to the manufacturer's instructions in 50 $\mu$ l volume containing approx 10ng of the pUC19 miniprep containing the V-region, 2% DMSO, 400 $\mu$ M dNTPs, 1 $\mu$ M each primer and buffer supplied. PCR was carried out as follows 1-95 °C 2 mins, 2-95°C 1 min, 3-56 °C 1 min, 4-72°C 1 min. Steps 2-4 30 cycles.

### 20 Cloning into expression vectors

The PCR products were purified using the MinElute PCR Purification kit from Qiagen according to manufacturer's instructions. The V<sub>H</sub> PCR product and RId (IgG2a) mammalian expression vector were digested Hind III-Spe I. The V<sub>L</sub> PCR product and Rln (k) mammalian expression vector were digested Hind III-BsiW I  
25 (NEB) according to manufacturer's instructions. Vectors were ligated to inserts in a 1:2 molar ratio using the Promega Quick Ligation kit. Ligation mixes were transfected into DH5a cells and colonies growing on ampicillin selection were grown up and sent for DNA sequence verification.

### Sequencing of recombinant anti-NOGO antibody 2A10/3

30 The sequence of the 2A10 heavy chain between the HindIII and EcoRI cloning sites was determined to be:



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AAGCTTGCCACCATGGGATGGAGCTGTATCATCCTCTTTTTGGTAGCAGC  
AGCTACAGGTGTCCACTCCCAGGTCCAAGTGCAGCAGCCTGGGACTGAAC  
TGGTGAAGCCTGGGGCTTCAGTGAAGCTGTCCTGCAAGGCTTCTGGCTAC  
ACCTTCACCAGCTACTGGATGCACTGGGTGAAGCAGAGGCCTGGACAAGG  
5 CCTTGAGTGGATTGGAAATATTAATCCTAGCAATGGTGGTACTAACTACA  
ATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACAAATCCTCCAGC  
ACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTA  
TTATTGTGAACTGGGACAGGGCTACTGGGGCCAAGGCACACTAGTCACCG  
TCTCCTCAGCCAAAACAACAGCCCCATCGGTCTATCCACTGGCCCCCTGTG  
10 TGTGGAGATACAAGTGGCTCCTCGGTGACTCTAGGATGCCTGGTCAAGGG  
TTATTTCCCTGAGCCAGTGACCTTGACCTGGAAGTCTGGATCCCTGTCCA  
GTGGTGTGCACACCTTCCCAGCTGTCCTGCAGTCTGACCTCTACACCCTC  
AGCAGCTCAGTGACTGTAACCTCGAGCACCTGGCCCAGCCAGTCCATCAC  
CTGCAATGTGGCCCACCCGGCAAGCAGCACCAAGGTGGACAAGAAAATTG  
15 AGCCCAGAGGGCCCAACATCAAGCCCTGTCCTCCATGCAATGCCCAGCA  
CCTAACCTCCTGGGTGGCCCATCCGTCTTCATCTTCCCTCCAAAGATCAA  
GGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGG  
ATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAAC  
GTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAG  
20 TACTCTCCGGGTGGTCAAGTGCCTTCCCCATCCAGCACCAGGACTGGATGA  
GTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAGACCTCCCAGCGCCC  
ATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGT  
ATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACCTC  
TGACCTGCATGGTCAACAGACTTCATGCCTGAAGACATTTACGTGGAGTGG  
25 ACCAACAACGGGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCCT  
GGACTCTGATGGTTCTTACTTTCATGTACAGCAAGCTGAGAGTGGAAAAGA  
AGAACTGGGTGGAAAGAAATAGCTACTCCTGTTTCAGTGGTCCACGAGGGT  
CTGCACAATCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAATG  
AGAATTC  
30 (SEQ ID NO:49)

The sequence of the 2A10 light chain between the HindIII and EcoRI cloning sites was determined to be:

AAGCTTGCCACCATGAGGTGCTCTCTTCAGTTTCTGGGGGTGCTTATGTT  
35 CTGGATCTCTGGAGTCAGTGGGGATAATTGTGATAACCCAGGATGAACTCT  
CCAATCCTGTCACTTCTGGAGAATCAGTTTCCATCTCCTGCAGGTCTAGT  
AAGAGTCTCCTATATAAGGATGGGAAGACATACTTGAATTGGTTTCTGCA  
GAGACCAGGACAATCTCCTCAGCTCCTGATCTATTTGATGTCCACCCGTG  
CATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGAACAGATTTT

ACCCTGGAAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTG  
 TCAACAACCTTGTAGAGTATCCGCTCACGTTTCGGTGCTGGGACCAAGCTGG  
 AGCTGAAACGTACGGATGCTGCACCGACTGTATCCATCTTCCCACCATCC  
 AGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAA  
 5 CTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCAGTGAAC  
 GACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAAGACAGC  
 ACCTACAGCATGAGCAGCACCCCTCACGTTGACCAAGGACGAGTATGAACG  
 ACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTTCACCCA  
 TTGTCAAGAGCTTCAACAGGAATGAGTGTTAAGAATTC  
 10 (SEQ ID NO:50)

**Example 5 - anti-NOGO-A antibody inhibits A $\beta$  40 and A $\beta$  42 peptide secretion from SHSY5Y-APPwt and SHSY5Yswe cells**

Figure 6 shows the dramatic reduction in levels of A $\beta$  40 and A $\beta$  42 peptide  
 15 secreted from SHSY5Y-APPwt cells expressing endogenous NOGO-A when the  
 anti-NOGO antibody 2A10 is introduced into the culture medium.

The effect is seen in a dose-dependent manner, at 30 $\mu$ g/ml reaching inhibition  
 levels of almost 90%. There is no apparent difference in the effect between A $\beta$   
 40 and A $\beta$  42 peptides (white bars and black bars respectively in figure 6), in  
 20 other words any effect of the anti-NOGO antibody on APP processing is not  
 preferential for either the A $\beta$  40 or A $\beta$  42 peptides.

Figure 7 shows the same experiment as in figure 6 but with an unrelated IgG1  
 antibody. As can clearly be seen in the figure, an unrelated (non anti-NOGO A)  
 monoclonal antibody has no inhibitory effect on the levels of A $\beta$  40 and A $\beta$  42  
 25 peptide secretion from the cells.

Figure 8 shows that the same unrelated IgG1 antibody similarly shows little or no  
 inhibitory effect on the levels of A $\beta$  40 and A $\beta$  42 peptide secretion from  
 SHSY5Y-APPswe cells expressing NOGO-A.

Similarly figure 9 shows the results of the same experiment as described above  
 30 for figure 6 but using an anti-NOGO monoclonal antibody which binds to NOGO-  
 A but is not a function-blocker (6D5). The non-function-blocking anti-NOGO-A  
 monoclonal antibody has minimal effect (less than 10%) on the secretion of A $\beta$   
 40 and A $\beta$  42 peptides from SHSY5Y-APPwt cells expressing NOGO-A. This

result suggests that the results shown in figure 6 are a result of the inhibition of NOGO functional activity by the anti-NOGO antibody.

Figure 10 shows the results of the same experiment as for figure 9, using the non-function blocking anti-NOGO monoclonal antibody (6D5) but with SHSY5Y-  
5 APPswe cells expressing endogenous NOGO-A. As before (figure 9) there is minimal effect on the levels of A $\beta$  40 and A $\beta$  42 being secreted by this cell line, being less than 10% inhibition.

Figure 11 shows the results of an experiment which extends the results of the experiment of figure 6. Figure 11 shows that the concentrate-dependent effect of  
10 the inhibitory effect shown by the function-blocking antibody 2A10/3 continues at a higher concentration, a level of greater than 90% inhibition being achieved at an antibody concentration of 50 $\mu$ g/ml.

Figure 12 shows the results of an identical experiment to that of figure 11 except that SHSY5Yswe cells are used. The concentration-dependent inhibitory effect  
15 of the antibody 2A10/3 continues to be seen at the higher concentration of 50 $\mu$ g/ml.

Figure 13 shows the effect of a different function-blocking anti-NOGO-A antibody, 2C4, on the secretion of A $\beta$  40 and A $\beta$  42 peptides from SHSY5Y-APPwt cells. The results show a concentration-dependent inhibitory effect on the levels of A $\beta$   
20 40 and A $\beta$  42 peptide secretion to a level of 36% at a concentration of 20 $\mu$ g/ml. Again the effect is seen on both A $\beta$  40 and A $\beta$  42 peptides.

Figure 14 compares the inhibitory effect of the anti-NOGO-A function-blocking antibodies 2A10, 2C4 and 15C3 (at the concentrations shown in the figure) with other control antibodies 10A4, IgG2b and 14D12. The figure shows that the  
25 effect on inhibition of A $\beta$  40 and A $\beta$  42 secretion is specific to the function-blocking anti-NOGO-A monoclonal antibodies.

**In the figures:**

Figure 1: NOGO A transfection leads to elevation of A $\beta$  40 peptide levels in SHSY5Y-APPwt cells

- 5    Figure 2: NOGO A transfection leads to elevation of A $\beta$  42 peptide levels in SHSY5Y-APPwt cells

Figure 3: Effect of NOGO A expression on A $\beta$  40 peptide levels

- 10   Figure 4: Effect of NOGO A expression on A $\beta$  42 peptide levels

Figure 5: Effect of NOGO A, NOGO-B and NOGO-C expression on A $\beta$  40 and A $\beta$  42

- 15   Figure 6. Anti-NOGO A antibody 2A10-BR inhibits A $\beta$  secretion from SHSY5Y-APPwt cells

Figure 7. Effect of Chemicon IgG1 on A $\beta$  secretion from SHSY5Y-APPwt cells

- 20   Figure 8. Effect of Chemicon IgG1 on A $\beta$  secretion from SHSY5Y-APPswe cells

Figure 9. Effect of control anti-NOGO (non function-blocking) antibody 6D5 on A $\beta$  secretion from SHSY5Y-APPwt cells

- 25   Figure 10. Effect of control anti-NOGO (non function-blocking) antibody 6D5 on A $\beta$  secretion from SHSY5Y-APPswe cells

Figure 11. Function-blocking anti-NOGO A monoclonal antibody 2A10 inhibits A $\beta$  secretion from SHSY5Y-APPwt cells

30

Figure 12. Function-blocking anti-NOGO A monoclonal antibody 2A10 inhibits A $\beta$  secretion from SHSY5Y-APPswe cells

Figure 13. Function-blocking anti-NOGO A monoclonal antibody 2C4 inhibits A $\beta$  secretion from SHSY5Y-APPwt cells

35

Figure 14. Effect of anti-NOGO A static culture antibody preparations and additional control antibodies on A $\beta$  secretion from SHSY5Y-APPwt cells. 2A10,

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2C4 and 15C3 are the static culture antibodies. All others are BR (Bioreactor) purified controls or commercially available controls.

**Claims**

1. A method of modulating production of an amyloidogenic peptide comprising contacting a cell which is expressing:
  - a) the precursor from which the amyloidogenic peptide is derived; and
  - 5 b) a NOGO polypeptide with a NOGO antagonist.
2. A method according to claim 1 wherein the precursor is APP.
- 10 3. A method according to claim 1 or 2 wherein the amyloidogenic peptide is A $\beta$ .
4. A method according to any one of claims 1 to 3 wherein the NOGO polypeptide is NOGO-A.
- 15 5. A method according to any one of claims 1 to 4 wherein the NOGO antagonist is a monoclonal antibody.
6. A method according to claim 5 wherein the monoclonal antibody is a  
20 function-blocking anti-NOGO-A monoclonal antibody.
7. Use of a NOGO antagonist in the manufacture of a medicament for the treatment or prophylaxis of a disease involving amyloidosis.
- 25 8. Use according to claim 7 wherein the amyloidosis is precipitated by an amyloidogenic peptide derived from APP.
9. Use according to claim 8 wherein the amyloidogenic peptide is A $\beta$ .
- 30 10. Use according to any one of claims 7 to 9 wherein the disease is Alzheimer's disease.
11. Use according to any one of claims 7 to 10 wherein the NOGO antagonist is a NOGO-A antagonist.
- 35 12. Use according to claim 11 wherein the NOGO-A antagonist is a monoclonal antibody.

13. Use according to claim 12 wherein the monoclonal antibody is a function-blocking anti-NOGO-A antibody.

14. Use according to claim 13 wherein the function-blocking anti-NOGO antibody is an antibody which binds to a region of human NOGO between 586 to 785 (NOGO-A amino acid numbering).

15. Use according to claim 12 wherein the anti-NOGO-A antibody comprises one or more of the following CDRs:

10 **Light chain CDRs**

<b>CDR</b>	<b>According to Kabat</b>
L1	RSSKSLLYKDGKTYLN (SEQ ID NO:1)
L2	LMSTRAS (SEQ ID NO:2)
L3	QQLVEYPLT (SEQ ID NO:3)

**Heavy chain CDRs**

<b>CDR</b>	<b>According to Kabat</b>
H1	SYWMH (SEQ ID NO:4)
H2	NINPSNGGTNYNEKFKS (SEQ ID NO:5)
H3	GQGY (SEQ ID NO:6)

15

16. Use according to claim 12 wherein the anti-NOGO-A antibody comprises one or more of the following CDRs:

**Light chain CDRs**

<b>CDR</b>	<b>According to Kabat</b>
L1	RSSQSLVHSNGNTYLH (SEQ ID NO:7)
L2	KVSNRFS (SEQ ID NO:8)
L3	SQSTHVPLT (SEQ ID NO:9)

20

**Heavy chain CDRs**

<b>CDR</b>	<b>According to Kabat</b>
H1	FSCYAMS (SEQ ID NO:10)
H2	SISDGGSYTYYPDNVKG (SEQ ID NO:11)
H3	ELLFDY (SEQ ID NO:12)

17. Use according to claim 12 wherein the anti-NOGO-A antibody comprises  
5 one or more of the following CDRs:

**Light chain CDRs**

<b>CDR</b>	<b>According to Kabat</b>
L1	RSSKSLHSHNGNTYLY (SEQ ID NO:13)
L2	RMSNLAS (SEQ ID NO:14)
L3	MQHLEYPLT (SEQ ID NO:15)

**Heavy chain CDRs**

10

<b>CDR</b>	<b>According to Kabat</b>
H1	SYWMN (SEQ ID NO:16)
H2	QIYPGDGDTNYNGKFKG (SEQ ID NO:17)
H3	VRFDY (SEQ ID NO:18)

15

18. Use according to claim 12 wherein the monoclonal antibody is a humanised antibody.

19. A method of treatment or prophylaxis of Alzheimer's disease which comprises administering to said human in need thereof an effective amount of an anti-NOGO antibody as defined in any one of claims 13 to 18.



**PB60607P**

**Abstract**

Methods of modulating production of an amyloidogenic peptide is disclosed. Use of such methods in the treatment of diseases involving amyloidosis, for example Alzheimer's disease, is also disclosed.

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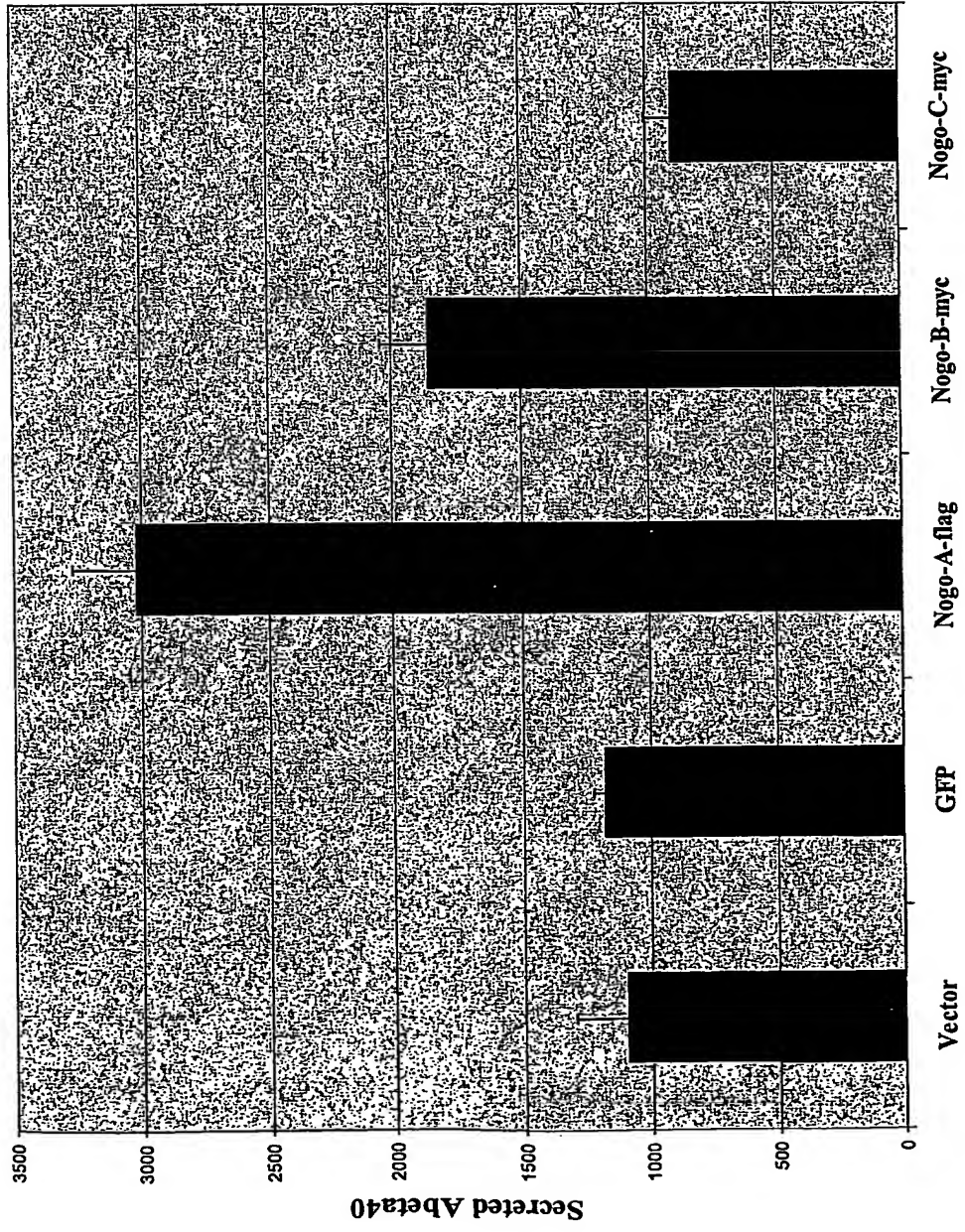


Figure 1

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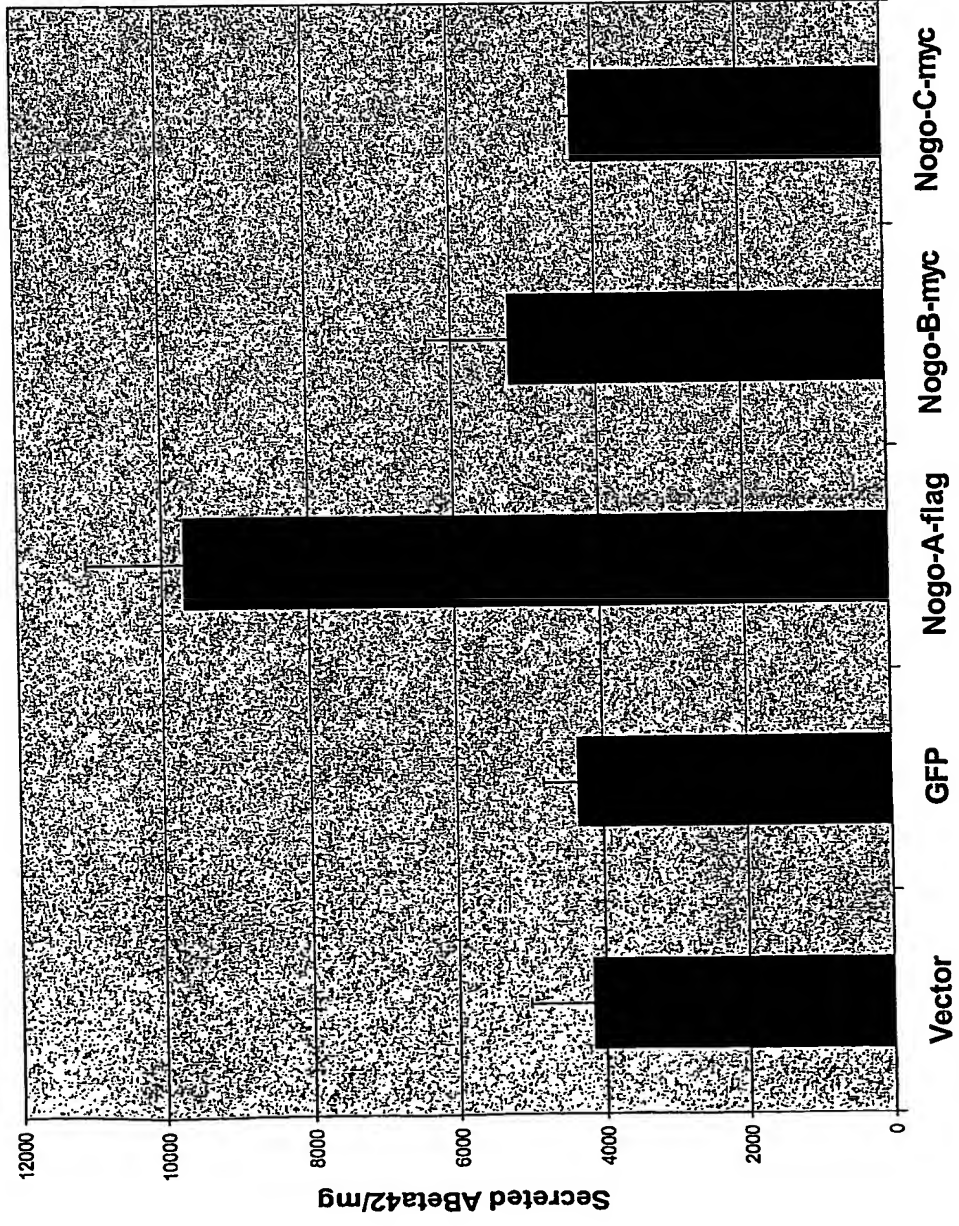


Figure 2

# Effect of NogoA Expression of Abeta40

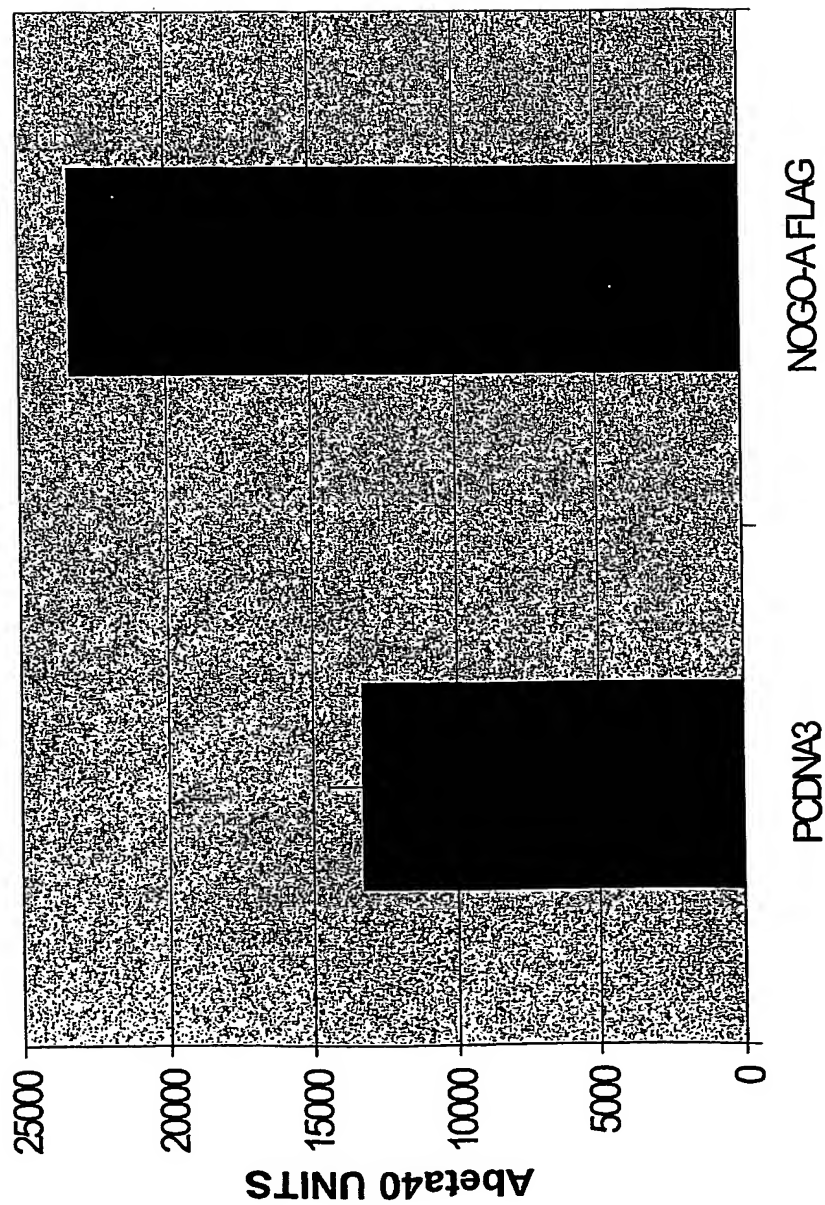


Figure 3

# Effect of Nogo on Abeta 42

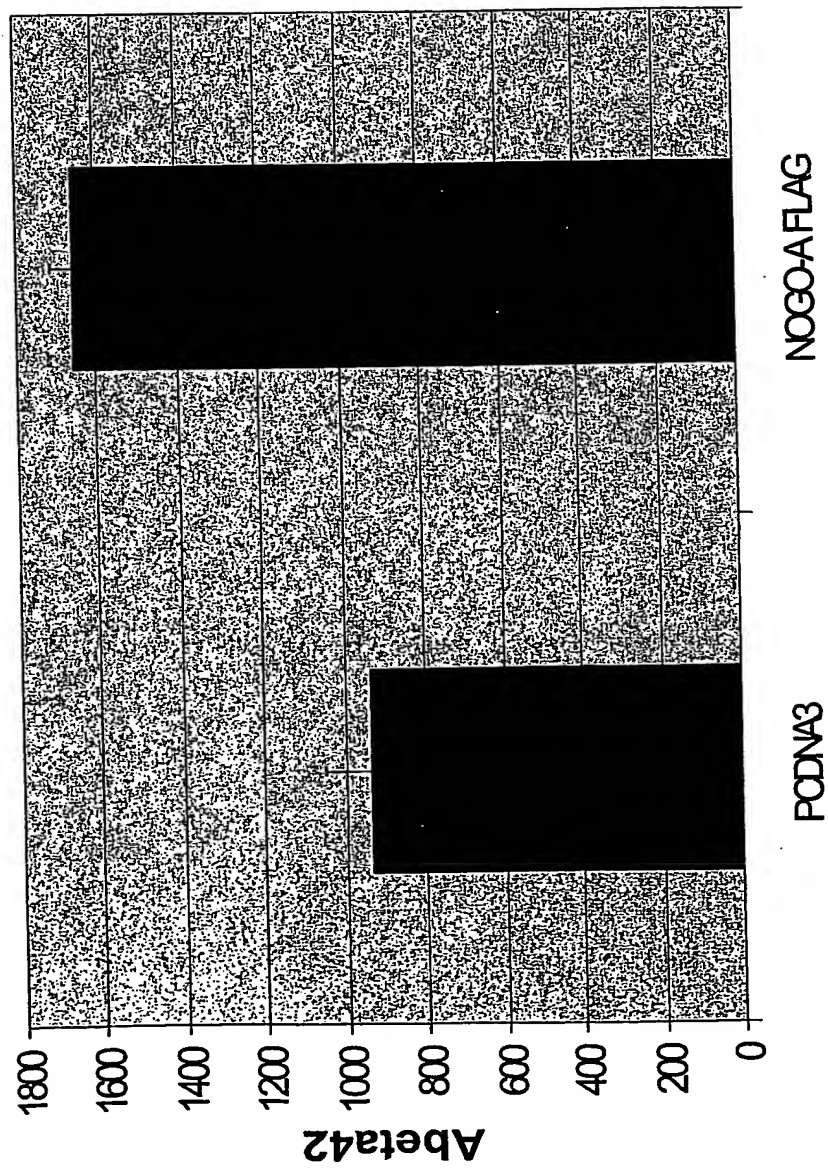


Figure 4

# Effect of Nogo Expression on Detected Abeta

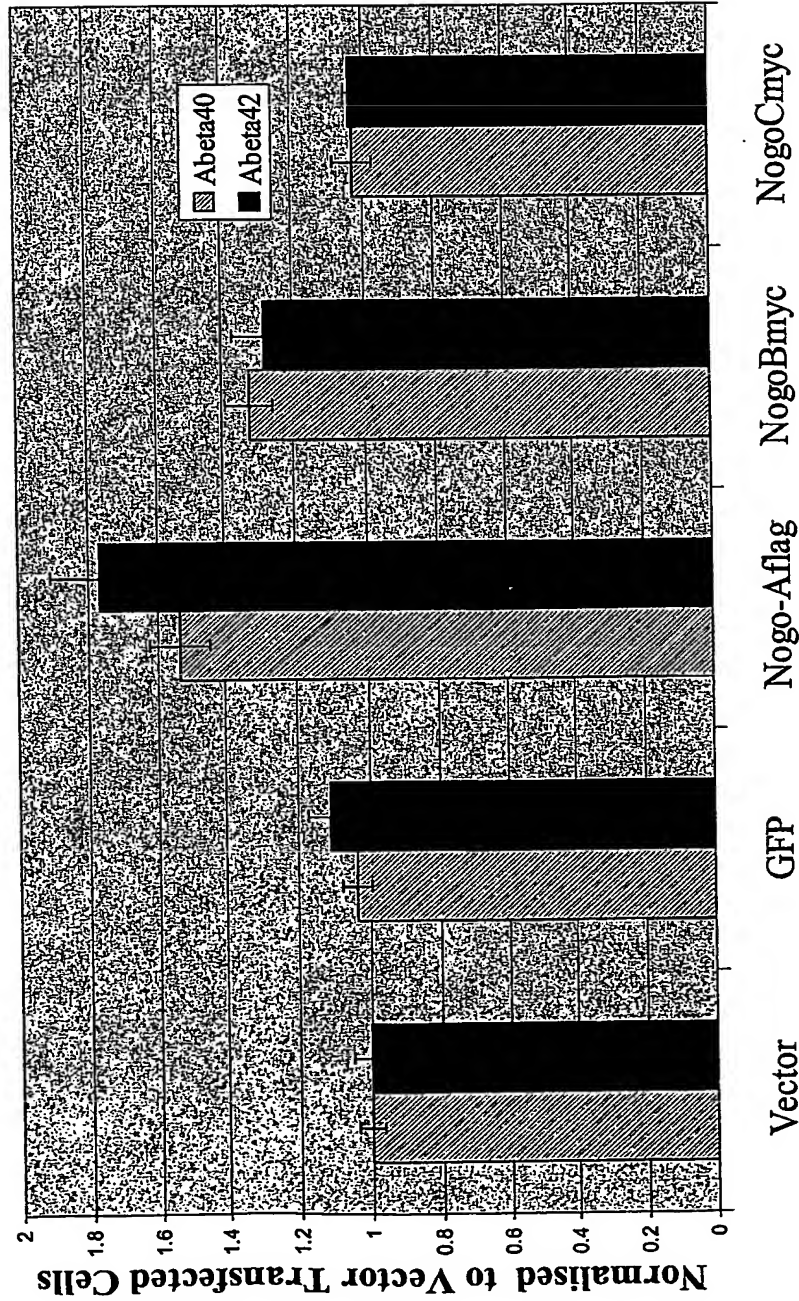
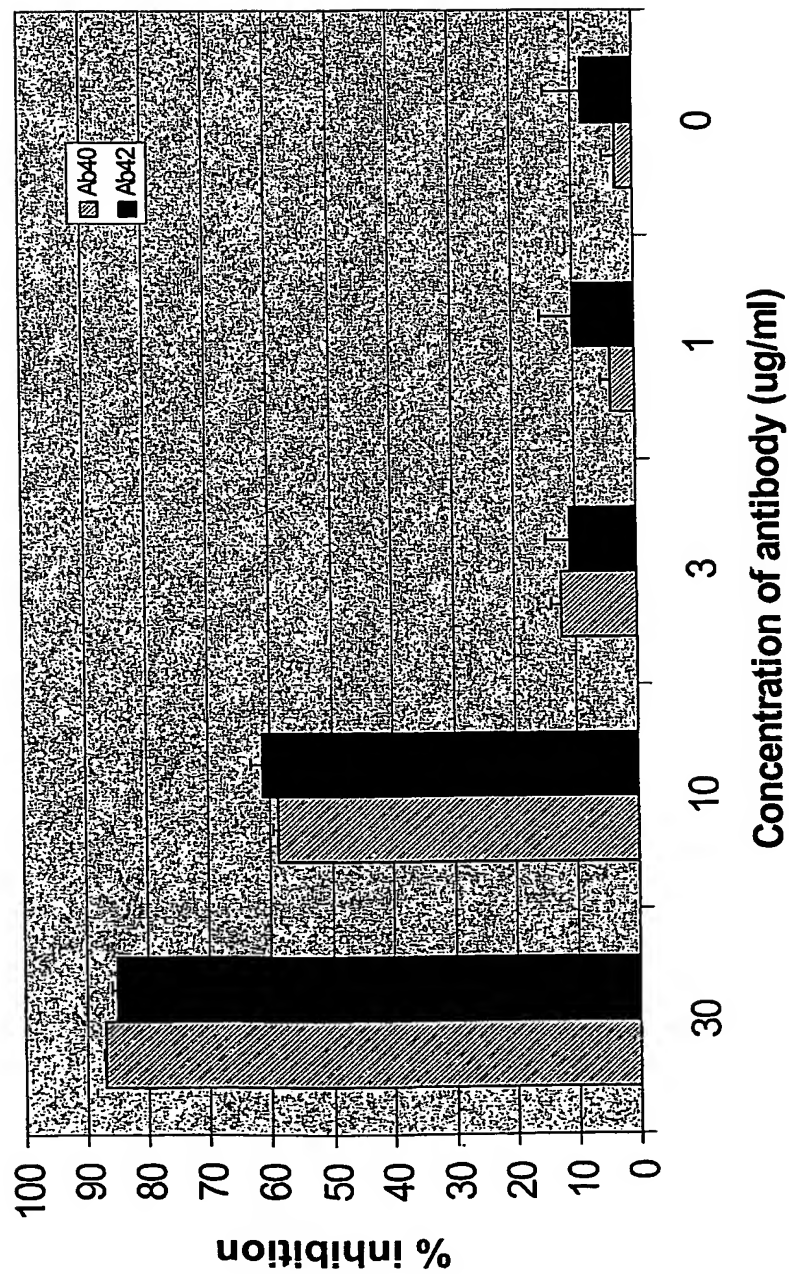


Figure 5



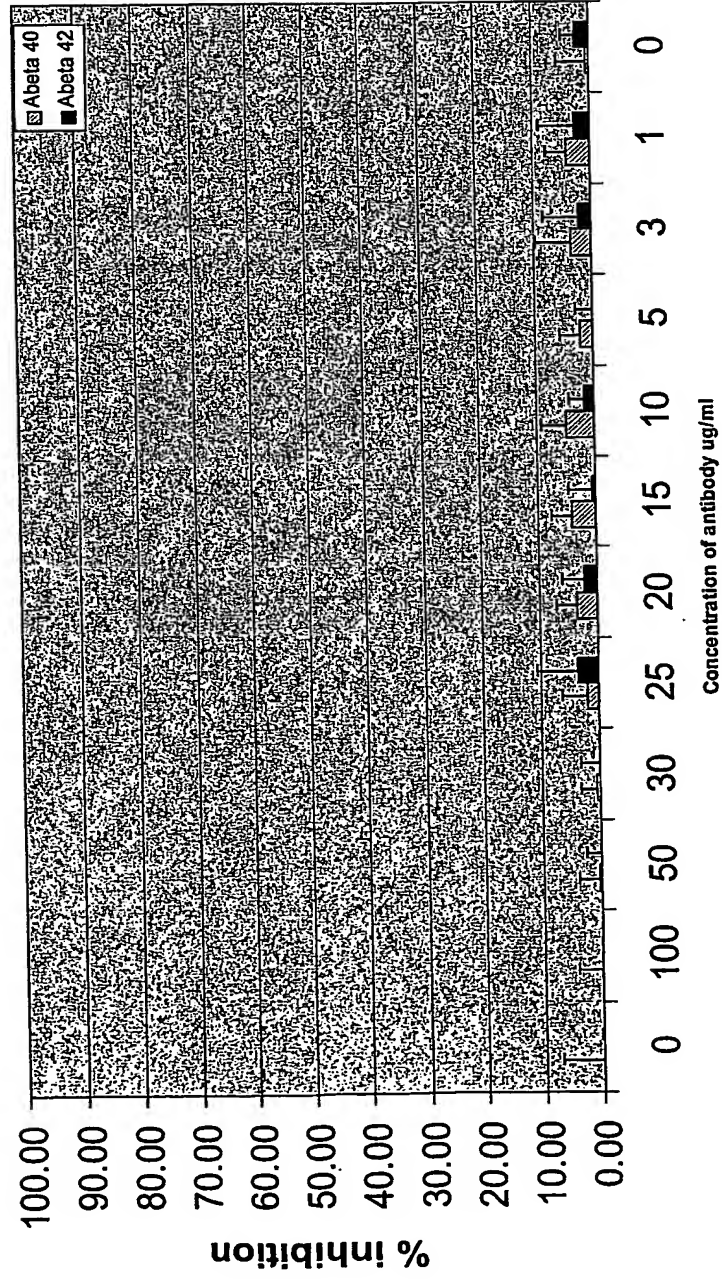
**Anti-Nogo A antibody 2A10-BR inhibits Abeta secretion  
from SHSY5Y-APPwt cells**



**Figure 6**

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**Effect of Chemicon IgG1 on Abeta secretion from SHSY5Y-APPwt cells**



**Figure 7**



# Effect of Chemicon mouse IgG1 on Abeta secretion from SHSY5Y-APPswe cells

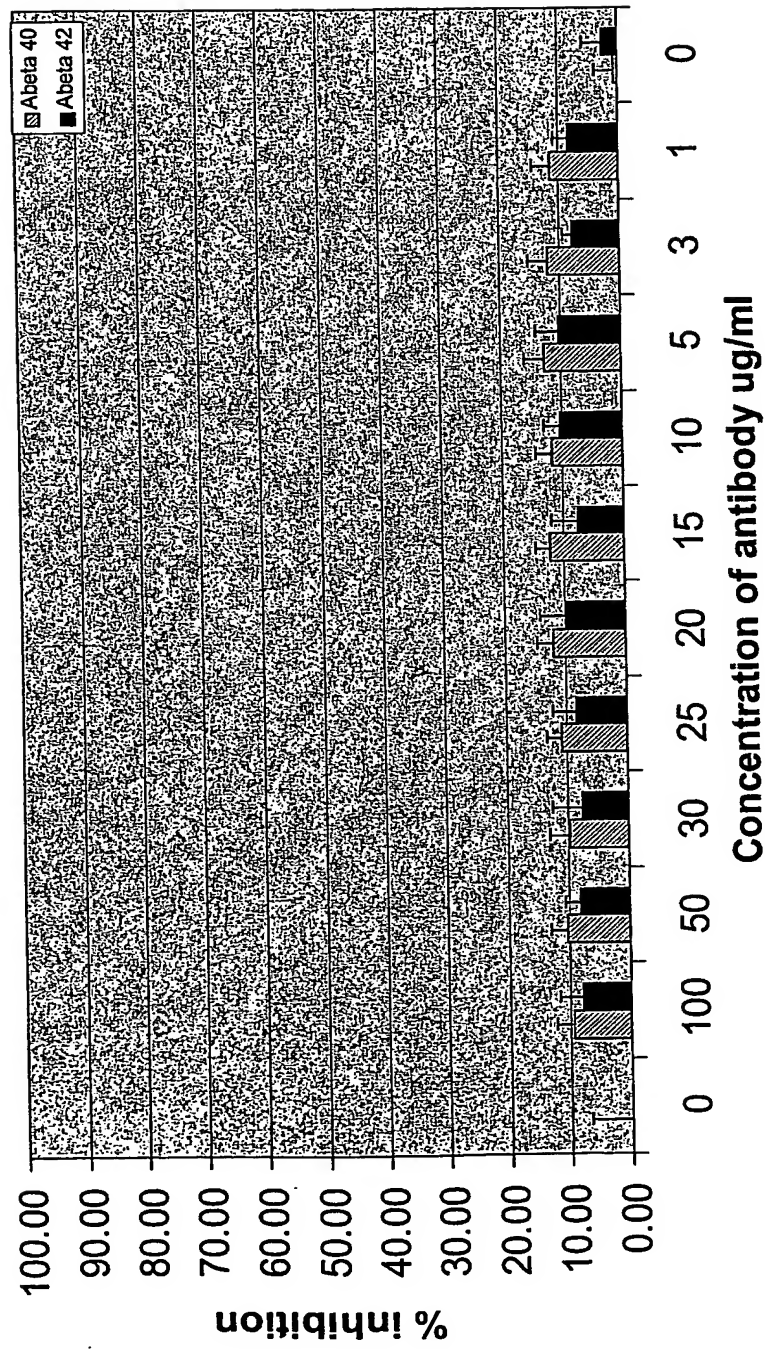


Figure 8

# Effect of Control Anti-Nogo-A monoclonal 6D5 on Abeta secretion from SHSY5Y-APPwt cells

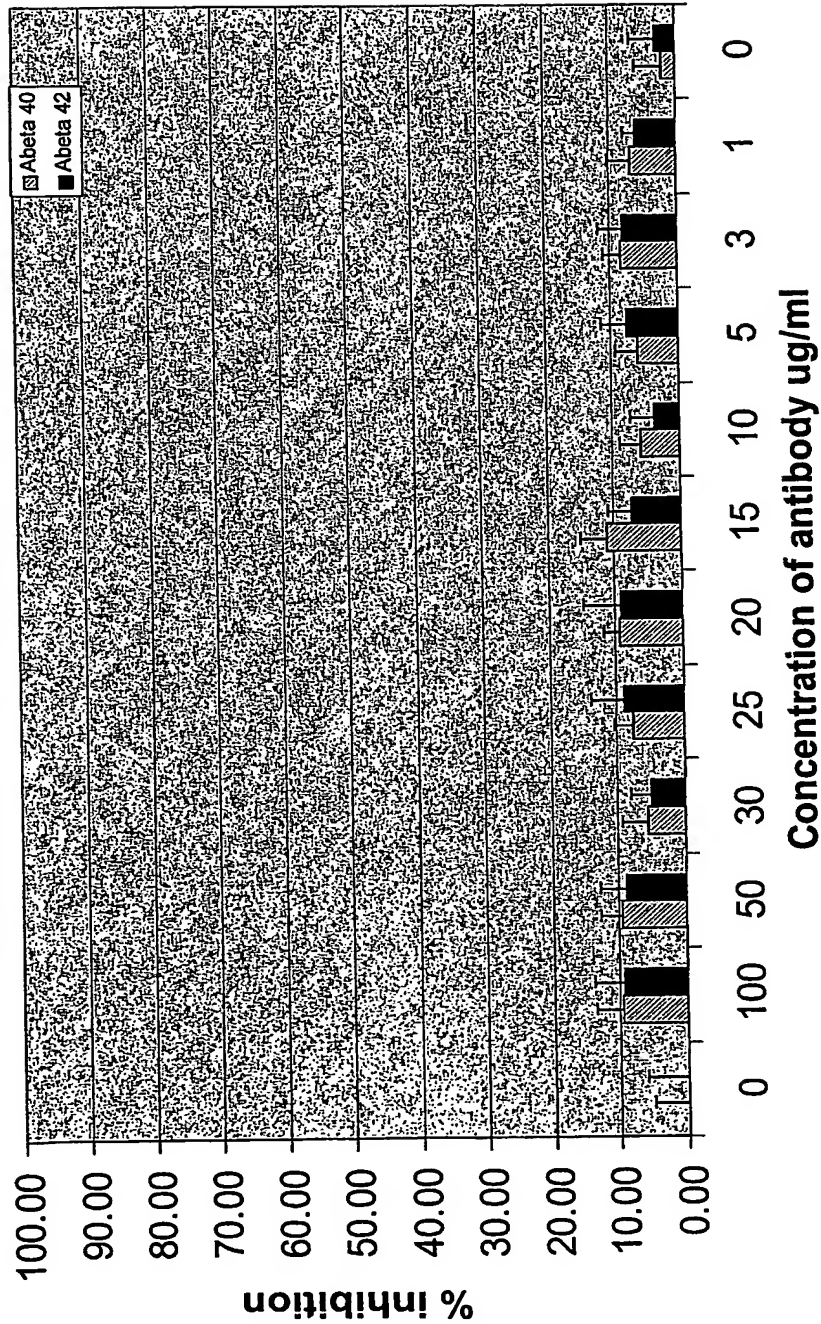


Figure 9

# Effect of Control Anti-Nogo-A monoclonal 6D5 on Abeta secretion from SHSY5Y-APPswe cells

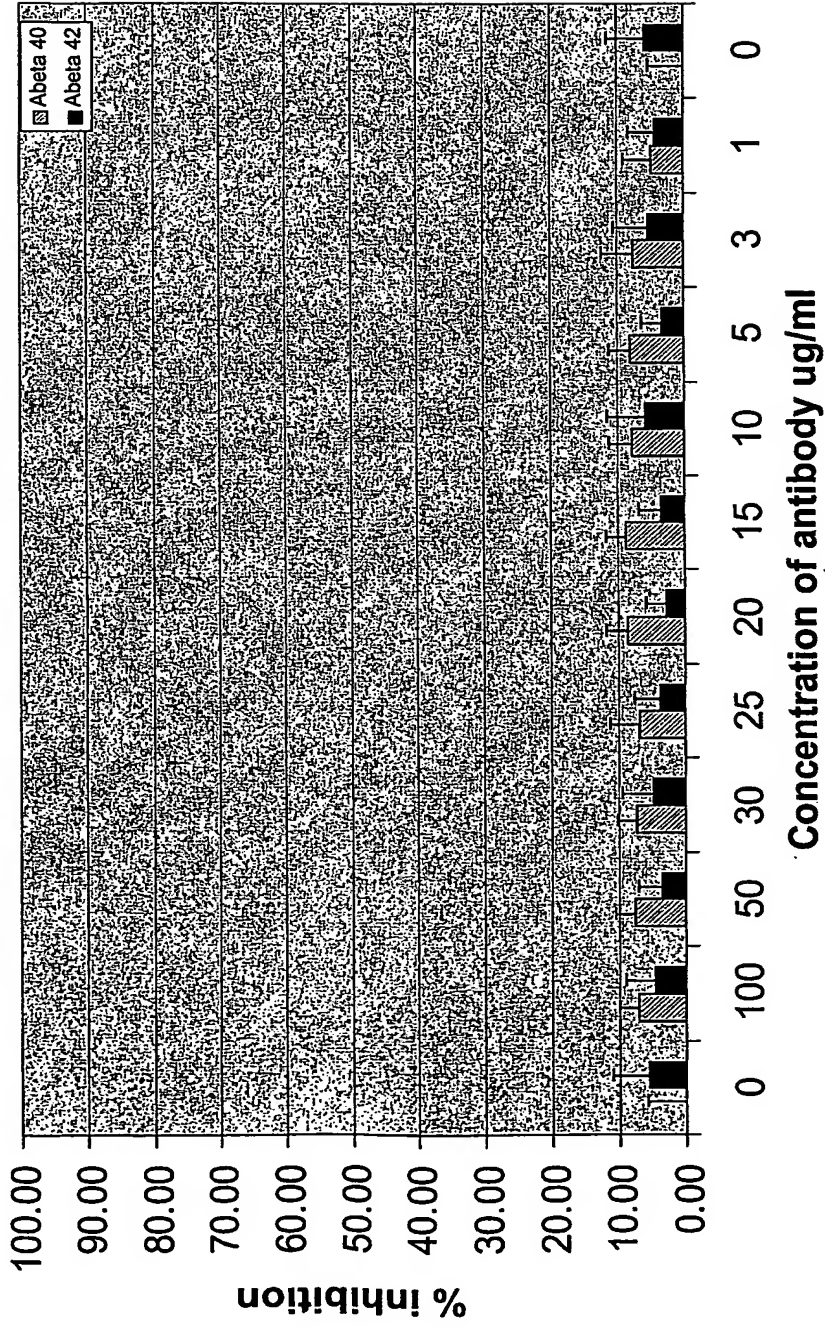


Figure 10

# Function Blocking Anti-Nogo-A monoclonal 2A10 inhibits Ab40/42 secretion from SHSY5Y-APPwt cells

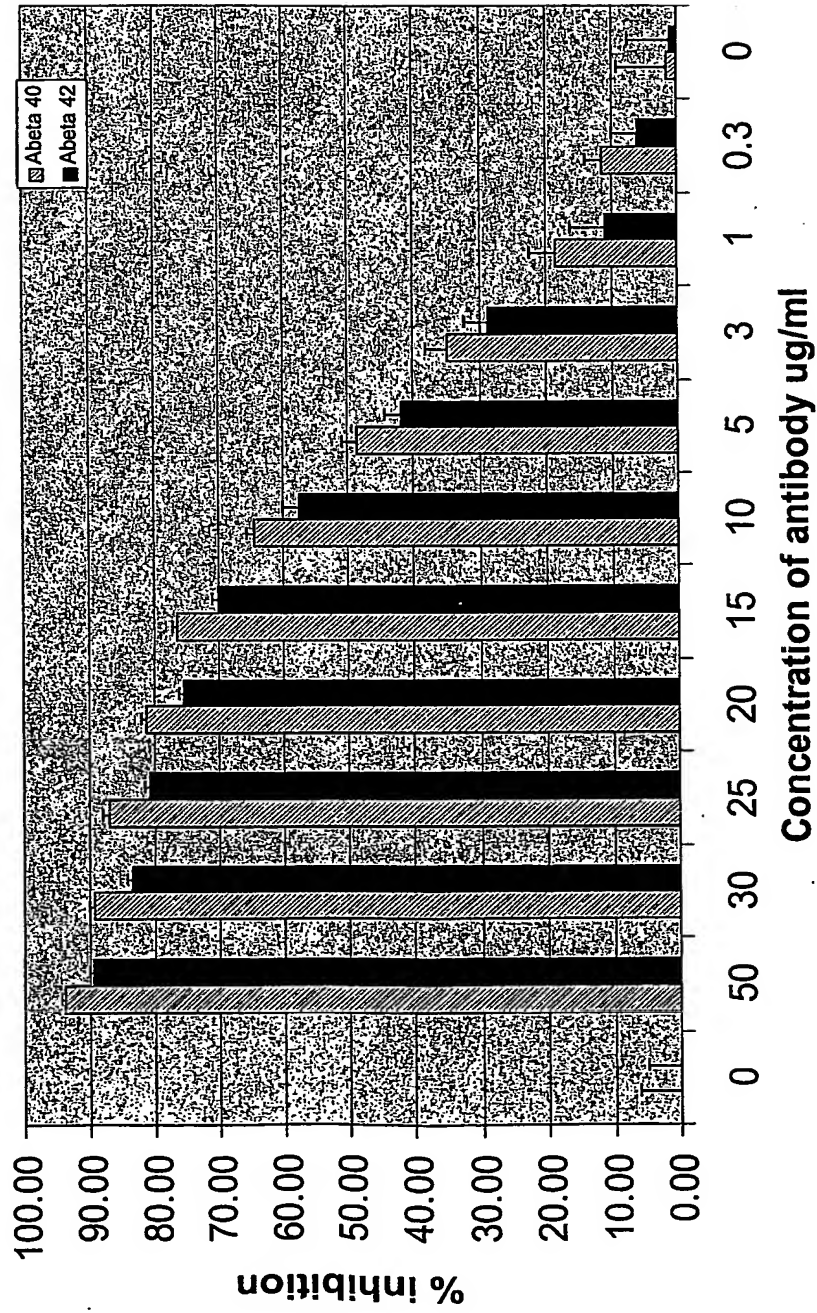


Figure 11

**Function Blocking Anti-Nogo-A monoclonal 2A10 inhibits  
Ab40/42 secretion from SHSY5Y-APPswe cells**

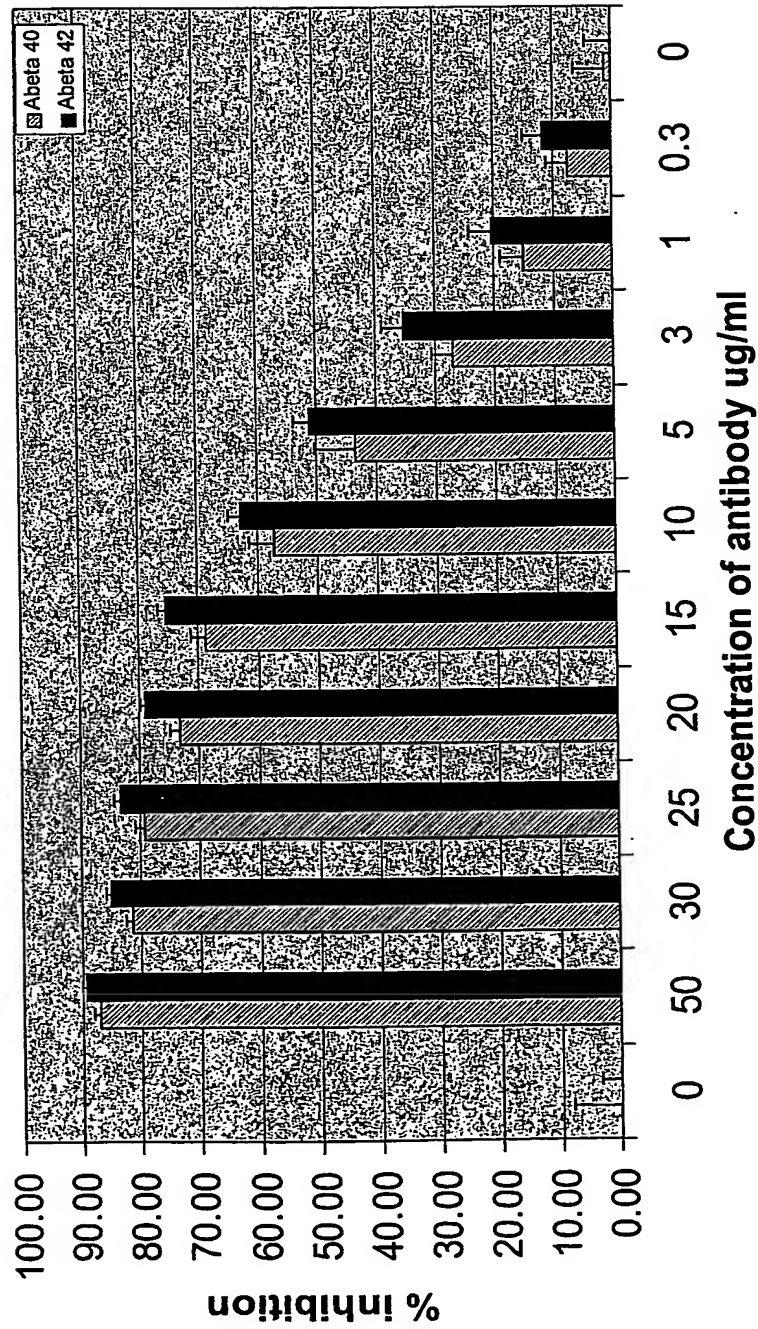
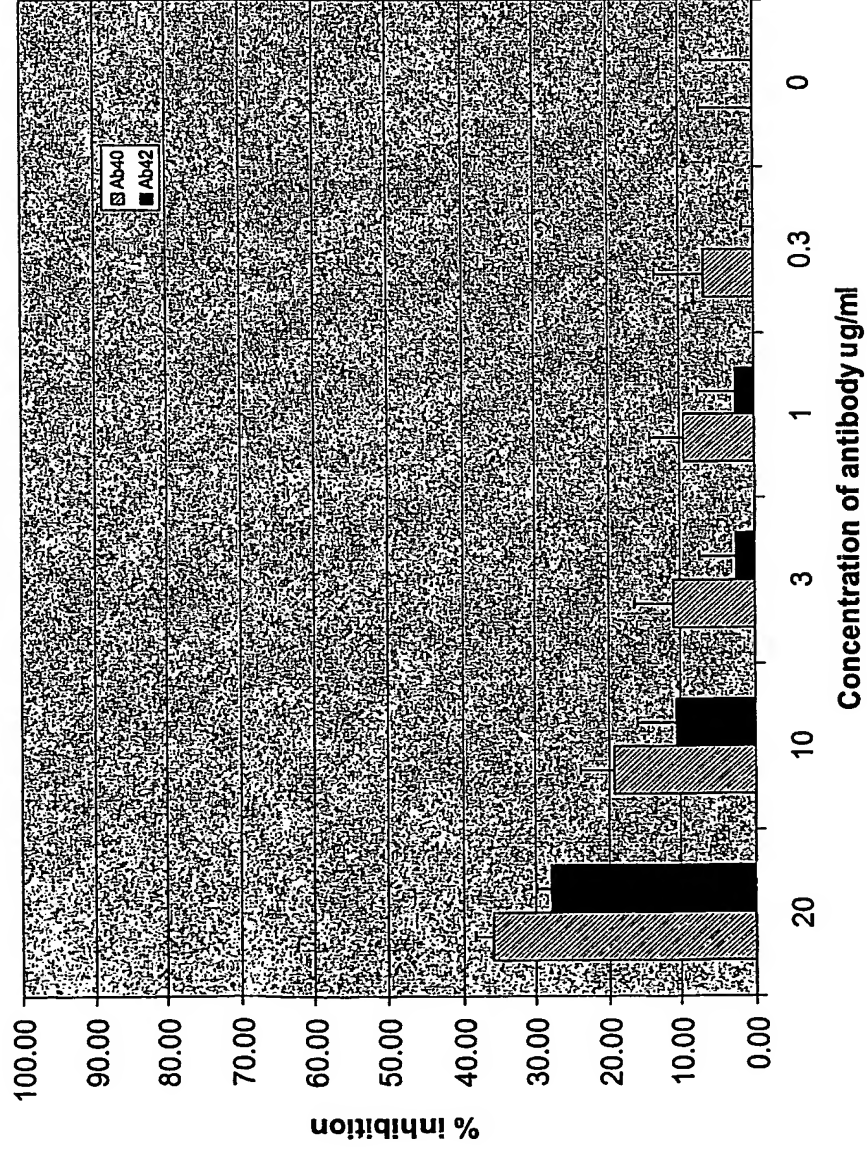


Figure 12



**Effect of Anti-Nogo-A 2C4-BR on Abeta secretion from SHSY5Y-APPwt cells**



**Figure 13**

# Effect of Anti-Nogo-A Static Culture Antibody Preparations and Additional Control antibodies on Abeta Secretion From SHSY5Y-APPwt Cells

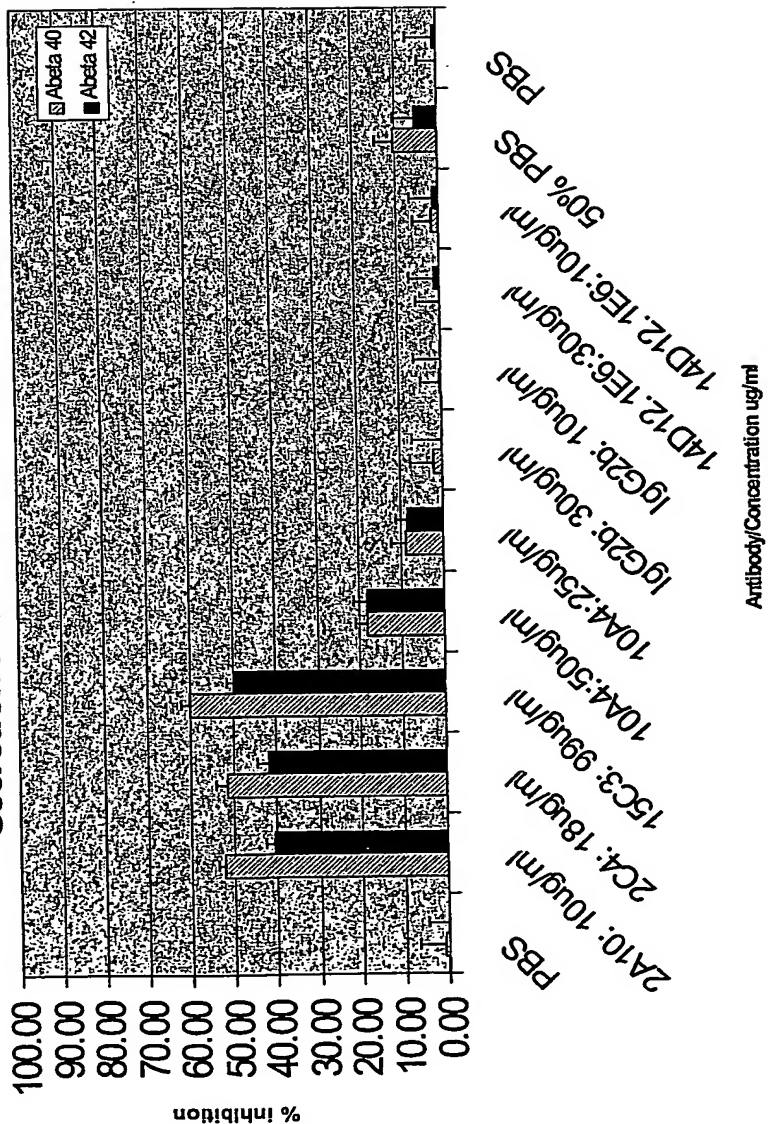
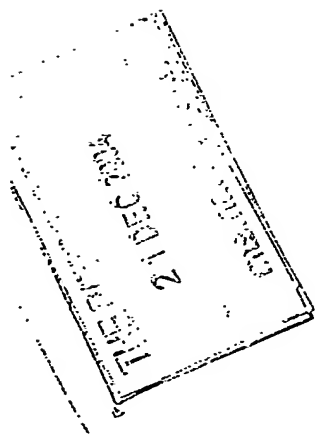


Figure 14



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